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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WALLACH, David
MALININ, Nikolai
BOLDIN, Mark
KOVALENKO, Andrei
METT, Igor
- (ii) TITLE OF INVENTION: MODULATORS OF TNF RECEPTOR ASSOCIATED
FACTOR (TRAF), THEIR PREPARATION AND USE
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
(B) STREET: 624 Ninth Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 09/155,676
(B) FILING DATE: 04-JAN-1999
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/IL97/00117
(B) FILING DATE: 01-APR-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: IL 117800
(B) FILING DATE: 02-APR-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: IL 119133
(B) FILING DATE: 26-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: BROWDY, Roger L.
(B) REGISTRATION NUMBER: 25,618
(C) REFERENCE/DOCKET NUMBER: WALLACH=21
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1906 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATTTGGGTCA CGCGGTGGCG GCGCTCTAGA ATAGTGGATC CCCCAGGGCTG CAGGAATTTCG 60
 ATTCGAGGCC ACGAAGGCCG GCGGCGCGGC GCANGCACCG GCCCGGGGAN AGGCNCCATG 120
 AGCGGATCNC NGAAACNATGA CAAAAGACAA TTTCTGCTGG AGCGACTGCT GGATGCAGTG 180
 AAACAGTSCC AGATCCGCTT TNGAGGGAGA AAGGAGATTG CCTCGGATTC CGACAGCAGG 240
 GTCACCTGTC TGTGTGCCCA GTTTGAAGCC GTCCTGCAGC ATGGCTTGAA GAGGAGTCGA 300
 GGATTGGCAC TCACAGCGGC AGCGATCAAG CAGGCAGCGG GCTTTGCCAG CAAAACCGAA 360
 ACAGAGCCCCG TGTCTTGTA CTACGTGAAG GAGGTCTCA ACAAGCACGA GCTGCAGCGC 420
 TTCTACTCCC TGCGCCACAT CGCCTCAGAC GTGGGCCGGG GTCGCGCCTG GCTGCGCTGT 480
 GCCCTCAACG AACACTCCCT GGAGCGCTAC CTGCACATGC TCCTGGCCGA CCGCTGCAGG 540
 CTGAGCACTT TTTATGAAGA CTGGTCTTTT GTGATGGATG AAGAAAGGTC CAGTATGCTT 600
 CCTACCATGG CAGCAGTCT GAACCTCCATA CTCTTTGCGA TTAACATCGA CAACAAGGAT 660
 TTGAACGGGC AGAGTAACTT TGCTCCACC GTTTCAGACC TCTTAAAGGA GTCAACGCAG 720
 AACGTGACCT CCTTGCTGAA GGAGTCCACG CAAGGAGTGA GCAGCCTGTT CAGGGAGATC 780
 ACAGCCTCCT CTGCCGTCT CATCCTCATC AAACCTGAAC AGGAGACCGA CCCTTGCTG 840
 TCGTGTCCAG GAATGTCAGT GCTGATGCCA AATGCAAAA GGAGCGGAAG AAGAAAAAGA 900
 AAGTGACCAA CATAATCTCA TTTGATGATG AGGAAGATGA GCAGAACTCT GGGGACGTGT 960
 TTAAAAAGAC ACCTGGGGCA GGGGAGAGCT CAGAGGACAA CTCCGACCGC TCCTCTGTCA 1020
 ATATCATGTC CGCCTTTGAA AGCCCTTCG GGCCTAACTC CAATGGAATC AGAGCAGCAA 1080
 CTCATGGAAA ATTGATTCCC TGTCTTTGAA CGGGGAGTTT GGGTACCAGA AGCTTGATGT 1140
 GAAAAGCATC GATGATGAAG ATGTGGATGA AAACGAAGAT GACGTGTATG GAAACTCATC 1200
 AGGAAGGAAG CACAGGGGCC ACTCGGATC GCCCGAGAAG CCACTGGAAG GGAACACCTG 1260
 CCTCTCCAG ATGCACAGCT GGGCTCCGCT GAAGGTGCTG CACAATGACT CCGACATCCT 1320
 CTTCCCTGTC AGTGGCGTGG GCTCCTACAG CCCAGCAGAT GCCCCCCTCG GAAGCCTGGA 1380
 GAACGGGACA GGACCAGAGG ACCACGTTCT CCCGATCCT GGACTTCGGT ACAGTGTGGA 1440
 AGCCAGCTCT CCAGGCCACG GAAGTCTCT GAGCAGCCTG TTAATTCTGC CTCAGTGCCA 1500
 GAGTCCATGA CAATTAGTGA ACTGCGCCAG GCGACTGTGG CCATGATGAA CAGGAAGGAT 1560
 GAGCTGGAGG AGGAGAACAG ATCACTGCGA AACCTGCTCG ACGGTGAGAT GGAGCACTCA 1620
 GCCGCGCTCC GGCAAGAGGT GGACACCTTG AAAAGGAAGG TGGCTGAACA GGAGGAGCGG 1680
 CAGGGCATGA AGGTCCAGGC GCTGGCCAGC TATCTTTGCT ATTTTGTGAG GAGATTCTAA 1740
 CCCACGTGA GAACCATGTG GTGGAGAAAT GGAGGGAGAG AGAAATCCAA CAGTTCCTGA 1800
 TAGTCTCATT TGAGCTCCTG GATCCAGTCT TTCCTGAAGC TGTGTTTCCT CTGGACTTTT 1860
 CATGTATGTG AGCCAATAAA TTGCTTTCAT TCCTTGAAAA AAAAAA 1906

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 604 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Thr Gly Pro Gly Xaa Gly Xaa Met Ser Gly Ser Xaa Asn Xaa Asp
 1 5 10 15
 Lys Arg Gln Phe Leu Leu Glu Arg Leu Leu Asp Ala Val Lys Gln Cys
 20 25 30
 Gln Ile Arg Phe Xaa Gly Arg Lys Glu Ile Ala Ser Asp Ser Asp Ser
 35 40 45
 Arg Val Thr Cys Leu Cys Ala Gln Phe Glu Ala Val Leu Gln His Gly
 50 55 60
 Leu Lys Arg Ser Arg Gly Leu Ala Leu Thr Ala Ala Ala Ile Lys Gln
 65 70 75 80
 Ala Ala Gly Phe Ala Ser Lys Thr Glu Thr Glu Pro Val Phe Trp Tyr
 85 90 95
 Tyr Val Lys Glu Val Leu Asn Lys His Glu Leu Gln Arg Phe Tyr Ser
 100 105 110
 Leu Arg His Ile Ala Ser Asp Val Gly Arg Gly Arg Ala Trp Leu Arg
 115 120 125
 Cys Ala Leu Asn Glu His Ser Leu Glu Arg Tyr Leu His Met Leu Leu
 130 135 140
 Ala Asp Arg Cys Arg Leu Ser Thr Phe Tyr Glu Asp Trp Ser Phe Val
 145 150 155 160
 Met Asp Glu Glu Arg Ser Ser Met Leu Pro Thr Met Ala Ala Gly Leu
 165 170 175
 Asn Ser Ile Leu Phe Ala Ile Asn Ile Asp Asn Lys Asp Leu Asn Gly
 180 185 190
 Gln Ser Lys Phe Ala Pro Thr Val Ser Asp Leu Leu Lys Glu Ser Thr
 195 200 205
 Gln Asn Val Thr Ser Leu Leu Lys Glu Ser Thr Gln Gly Val Ser Ser
 210 215 220
 Leu Phe Arg Glu Ile Thr Ala Ser Ser Ala Val Ser Ile Leu Ile Lys
 225 230 235 240
 Pro Glu Gln Glu Thr Asp Pro Cys Leu Ser Cys Pro Gly Met Ser Val
 245 250 255
 Leu Met Pro Asn Ala Lys Arg Ser Gly Arg Arg Lys Arg Lys Xaa Pro
 260 265 270
 Thr Xaa Ser His Leu Met Met Arg Lys Met Ser Arg Thr Leu Gly Thr
 275 280 285
 Cys Leu Lys Arg His Leu Gly Gln Gly Arg Ala Gln Arg Thr Thr Pro
 290 295 300
 Thr Ala Pro Leu Ser Ile Ser Cys Pro Pro Leu Lys Ala Pro Ser Gly

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(2) INFORMATION FOR SEQ ID NO: 3:

(A) LENGTH: 2631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCTCTCAC AGCCCAGGCC ATCCAAGAGG GGCTGAGGAA AGAGCCCATC CACCGCGTGT 60
 CTGCAGCGGA GCTGGGAGGG AAGGTGAACC GGGCACTACA GCAAGTGGGA GGTCTGAAGA 120
 GCCCTTGGAG GGGAGAATAT AAAGAACCAA GACATCCACC GCCAAATCAA GCCAATTACC 180
 ACCAGACCCT CCATGCCCAG CCGAGAGAGC TTTCGCCAAG GGCCCCAGGG CCCCGGCCAG 240
 CTGAGGAGAC AACAGGCAGA GCCCCTAAGC TCCAGCCTCC TCTCCCACCA GAGCCCCCAG 300
 AGCCAAACAA GTCTCTTCCC TTGACTTTGA GCAAGGAGGA GTCTGGGATG TGGGAACCCT 360
 TACCTCTGTC CTCCCTGGAG CCAGCCCCCTG CCAGAAACCC CAGCTCACCA GAGCGGAAAG 420
 CAACCGTCCC GGAGCAGGAA CTGCAGCAGC TGGAAATAGA ATTATTCTCT AACAGCCTGT 480
 CCCAGCCATT TTCTCTGGAG GAGCAGGAGC AAATTCTCTC GTGCCTCAGC ATCGACAGCC 540
 TCTCCCTGTC GGATGACAGT GAGAAGAACC CATCAAAGGC CTCTCAAAGC TCGCGGGACA 600
 CCCTGAGCTC AGGCGTACAC TCCTGGAGCA GCCAGGCCGA GGCTCGAAGC TCCAGCTGGA 660
 ACATGGTGCT GGCCCGGGGG CGGCCACCG ACACCCCAAG CTATTTCAAT GGTGTGAAAG 720
 TCCAAATACA GTCTCTTAAT GGTGAACACC TGCACATCCG GGAGTTCCAC CGGGTCAAAG 780
 TGGGAGACAT CGCCACTGGC ATCAGCAGCC AGATCCCAGC TGCAGCCTTC AGCTTGGTCA 840
 CCAAAGACGG GCAGCCTGTT CGCTACGACA TGGAGGTGCC AGACTCGGGC ATCGACCTGC 900
 AGTGCACACT GGCCCTGAT GGCAGCTTGG CCTGGAGCTG GAGGGTCAAG CATGGCCAGC 960
 TGGAGAACAG GCCCTAACCC TGCCCTCCAG CGCCGGCTCC AACTGCCCG AAAGCAGCCT 1020
 TCCTGCTCGG TGCACGATGC TGCCCTGAAA ACACAGGCTC AGCCGTTCCT AGGGGATYTG 1080
 NCCAGCCCC CGGCTCARCA GNTGGGAACC AGGGCCTCGN CAGCNAGCNA AGGTNGGGGG 1140
 CAAGCNAGAA TGCCTCCAG GATTTACAN CCTGAGCCCN TGCCCCANCC CTGCTGAADA 1200
 AAACAYTNCC GCCACGTGAA GAGACAGAAG GAGGATGGNC AGGAGTTNNA CCTYGGGGAA 1260
 ACAAACAGG GATCTTTNTT CTGCCCCTGC TCCAGTNCGA GTTGGCCTGN ACCCGCTTGG 1320
 ANTCAGTGAC CATTTGTTGG CAGANCAGGG GAGAGCAGCT TCCAGCCTGG GTCAGAAGGG 1380
 GTGGGCGAGC CCTTCGGCCC CTCACCTNC CAGGCTGCTG TGNAGAGTGT CAAGTGTGTA 1440
 AGGGNCCCAA ANCTCAGGNT TCAGTGAGA ACCAGGTNCA GCAGGTATGC CCGCCGNTA 1500
 GGTAAANNNG GGGCCCTCTN AAACCCCTTG CCTNGGCCTN CACCTNGGCC AGCTCANCCC 1560
 CTTTTGGGTG TAGGGGAAAA GAATGCCTGA CCCTGGGAAG GCTWCCCTGG TAGAATACAC 1620
 CACACTTTTC AGGTTGTTGC AACACAGGTC CTGAGTTGAC CTCTGGTTCA GCCAAGGACC 1680
 AAAGAAGGTG TGTAAGTGAA GTGGTTCTCA GTNCCCAGA CATGTGCCCC TTTGCTGCTG 1740
 GCTACCACTC TTCCCCAGAG CAGCAGGCC CGAGCCCCTT CAGGCCCAGC ACTGCCCCAG 1800
 ACTCGCTGGC ACTCAGTTCC CTCATCTGTA AAGGTGAAGG GTGATGCAGG ATATGCCTGA 1860
 CAGGAACAGT CTGTGGATGG ACATGATCAG TGCTNAAGGN AAAGCAGCAG AGAGAGACGY 1920
 TCCGGCGCCC CAGNCCCCAC TNATCAGTGT NCCAGCGTGC TNGGTTNCCC CAGNAGCACA 1980
 GCTNCAGNCA TCANCACTGA CACTNCACCC TNGCCCTGCC CCTNGGCCAN GAGGGTACTG 2040

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CCGNACGGCA CTTTGCACNT CTGATGNACC TCAAAGCACT TTCATGGCTN GCCCTCTNNG 2100
 GCAGGGNCAG GGNACAGGNC AGTGACANCT GTAGGNAGCA TANGCAANGC CAGGAGATGG 2160
 GGTGNAAGGG ANCACAGTCT TGAGCTGTCC ANCATGCATG TGACTNCCTC AAACCTCTTN 2220
 NCCAGNATTT CTCTAAGAAT AGCANCCCCC TTNCCCCATT GCCCCAGCTT AGCCTCTTCT 2280
 CCCAGGGGAG CTANCTCAGG ACTCACGTAG CATTAAATCA GCTGTGNAAT CGTCAGGGGG 2340
 TGTCTGCTAG CCTCAACCTC CTGGGGCAGG GGACGCCGAG ACTCCGTGGG AGAAGCTCAT 2400
 TCCCACATCT TGCCAAGACA GCCTTTNGTC CAGCTGTCCA CATTGAGTCA GACTGCTCCC 2460
 GGGGAGAGAG CCCCCGCCCC CAGCACATAA AGAACTGCAG CCTTGGTACT GCAGAGTCTG 2520
 GTTGTAGAG AACTCTTTGT AAGCAATAAA GTTTGGGGTG ATGACAAATG TTAACAAAAG 2580
 GCCTTCGTGG CCTCGAATCA AGCTTATCGA TACCGTCGAC CTCGAGGGGG G 2631

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATTGGAGTC ACGCGGTGGC GCGCTCTAG AATAGTGGAT CCCCCGGCTG CANGGAATTC 60
 GATTGAGACC CACGAAGGCC CCTTCTTCTG TGGTCGCGGC ACCTTTACAG CCGCAAGCAC 120
 CCAGCGGCAG CTGAAGGAGG CTTTGTAGAG GCTCTGCCC CAGGTGGAGG CGCCCCGCAA 180
 GGCCATCCGC GCCGCTCAGG TGGAGCGCTA TGTGCCCGAA CACGAGCGAT GCTGCTGGTG 240
 CCTGTGCTGC GGCTGTGAGG TGCGGGAACA CCTGAGCCAT GGAAACCTGA CGGTGCTGTA 300
 CGGGGGGCTG CTGGAGCATC TGGCCAGCCC AGAGCACAAG AAAGCAACCA ACAAATTCTG 360
 GTGGGAGAAC AAAGCTGAGG TCCAGATGAA AGAGAAGTTT CTGGTCACTC CCCAGGATTA 420
 TGC GCGATT C AAGAAATCCA TGGTGAAAGG TTTGGATTCC TATGAAGAAA AGGAGGATAA 480
 AGTGATCAAG GAGATGGCAG CTCAGATCCG TGAGGTGGAG CAGAGCCGAC AGGAGGTGGT 540
 TCGGTCTGTC TTAGAGCCTC AGGCAGTGCC AGACCCAGAA GAGGGCTCTT CAGCACCTAG 600
 AAGCTGGAAA GGGATGAACA GCCAAGTAGC TTCCAGCTTA CAGCAGCCCT CAAATTTGGA 660
 CCTGCCACCA GCTCCAGAGC TTGACTGGAT GGAGACAGGA CCATCTCTGA CATTCAATTGG 720
 CCATCAGGAT ATACCAGGAG TTGGTAACAT CCACTCAGGT GCCACACCTC CCTGGATGAT 780
 CCAAGATGAA GAATACATTG CTGGGAACCA AGAAATAGGA CCATCTCTATG AAGAATTTCT 840
 TAAAGAAAAG GAAAAACAGA AGTTGAAAAA ACTCCCCCA GACCGAATTG GGGCCAACTT 900
 TGATCACAGC TCCAGGACCA GTGCAGGCTG GCTGCCCTCT TTTGGGCGGC GTCTGGAATA 960
 ATGGACGCCG CTGGCAGTCC AGACATCAAC TCCAAACTG AAGCTGCAGC AATGAAGAAG 1020
 CAGTCACATA CAGAAAAAAG CTAATCATGC TCTCTACCAA CTACCATGAG GCTAAAAGCC 1080

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AAAGTCAACC AAACCCCTAT TATACCTTCC ACCCAAATTC TTTATCATTG TCTTTCTTAG 1140
 GAAACAGACA TACTCATTCA TTTGATTTAA TAAAGTTTAA TTTTTCGGCC TTCGTGGCCT 1200
 CGAATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGC CGTACCCACT TTT 1253

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ile Gly Val Thr Arg Trp Arg Arg Ser Arg Ile Val Asp Pro Arg Ala
 1 5 10 15
 Ala Xaa Asn Ser Ile Arg Ala His Glu Gly Pro Phe Phe Cys Gly Arg
 20 25 30
 Gly Thr Phe Thr Ala Ala Ser Thr Gln Arg Gln Leu Lys Glu Ala Phe
 35 40 45
 Glu Arg Leu Leu Pro Gln Val Glu Ala Ala Arg Lys Ala Ile Arg Ala
 50 55 60
 Ala Gln Val Glu Arg Tyr Val Pro Glu His Glu Arg Cys Cys Trp Cys
 65 70 75 80
 Leu Cys Cys Gly Cys Glu Val Arg Glu His Leu Ser His Gly Asn Leu
 85 90 95
 Thr Val Leu Tyr Gly Gly Leu Leu Glu His Leu Ala Ser Pro Glu His
 100 105 110
 Lys Lys Ala Thr Asn Lys Phe Trp Trp Glu Asn Lys Ala Glu Val Gln
 115 120 125
 Met Lys Glu Lys Phe Leu Val Thr Pro Gln Asp Tyr Ala Arg Phe Lys
 130 135 140
 Lys Ser Met Val Lys Gly Leu Asp Ser Tyr Glu Glu Lys Glu Asp Lys
 145 150 155 160
 Val Ile Lys Glu Met Ala Ala Gln Ile Arg Glu Val Glu Gln Ser Arg
 165 170 175
 Gln Glu Val Val Arg Ser Val Leu Glu Pro Gln Ala Val Pro Asp Pro
 180 185 190
 Glu Glu Gly Ser Ser Ala Pro Arg Ser Trp Lys Gly Met Asn Ser Gln
 195 200 205
 Val Ala Ser Ser Leu Gln Gln Pro Ser Asn Leu Asp Leu Pro Pro Ala
 210 215 220
 Pro Glu Leu Asp Trp Met Glu Thr Gly Pro Ser Leu Thr Phe Ile Gly
 225 230 235 240
 His Gln Asp Ile Pro Gly Val Gly Asn Ile His Ser Gly Ala Thr Pro
 245 250 255
 Pro Trp Met Ile Gln Asp Glu Glu Tyr Ile Ala Gly Asn Gln Glu Ile

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 Cont

	260		265		270
Gly Pro Ser	Tyr Glu Glu Phe	Leu Lys Glu Lys Glu Lys	Gln Lys Leu		
275		280	285		
Lys Lys Leu Pro	Pro Asp Arg Val Gly Ala Asn Phe	Asp His Ser Ser			
290	295	300			
Arg Thr Ser Ala	Gly Trp Leu Pro Ser Phe	Gly Pro Arg Leu Glu Xaa			
305	310	315	320		
Trp Thr Pro Leu	Ala Val Gln Thr Ser Thr	Pro Lys Leu Lys Leu Gln			
	325	330	335		
Gln Xaa Arg Ser	Ser His Ile Gln Lys Lys Ala Asn His	Ala Leu Tyr			
340	345	350			
Gln Leu Pro Xaa	Gly Xaa Lys Pro Lys Ser Thr Lys	Pro Leu Leu Tyr			
355	360	365			
Leu Pro Pro Lys	Phe Phe Ile Ile Val Phe Leu Arg	Lys Gln Thr Tyr			
370	375	380			
Ser Phe Ile Xaa	Phe Asn Lys Val Leu Phe	Phe Gly Leu Arg Gly Leu			
385	390	395	400		
Glu Ser Ser Leu	Ser Ile Pro Ser Thr Ser	Arg Gly Gly Arg Thr His			
	405	410	415		

Phe

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AGCGGGGGGA CTGTGCCGTG TGGAACGTGT AGCTGTTGAA GGTGGACTCT GTTACCATTG 60

AGGATGTTTG GAGGATGAGT ATGTGTGGCA GAGGCACACA TAAACAGGCA GAGACCCTTT 120

GCCCCTGCCT TTCTCCCCCA ACCCAAGGCT GACCTGTGTT CTCCCAGGTC TGGGATTCTA 180

AGTGACCTGC TCTGTGTTTG GTCTCTCTCA GGATGAGCAC AAGCCTGGGA GATGGCAGTG 240

ATGGAAATGG CCTGCCAGG TGCCCTGGC TCAGCAGTGG GGCAGCAGAA GGAAC TCCCC 300

AAGCCAAAGG AGAAGACGCC GCCACTGGGG AAGAAACAGA GCTCCGTCTA CAAGCTTGAG 360

GCCGTGGAGA AGAGCCCTGT GTTCTGCGGA AAGTGGGAGA TCCTGAATGA CGTGATTACC 420

AAGGGCACAG CCAAGGAAGG CTCCGAGGCA GGGCCAGCTG CCATCTCTAT CATCGCCCAG 480

GCTGAGTGTG AGAATAGCCA AGAGTTCAGC CCCACCTTTT CAGAACGCAT TTTCATCGCT 540

GGGTCCAAAC AGTACAGCCA GTCCGAGAGT CTTGATCAGA TCCCCAACAA TGTGGCCCAT 600

GCTACAGAGG GCAAAATGGC CCGTGTGTGT TGGAAGGGAA AGCGTCGCAG CAAAGCCCGG 660

AAGAAACGGA AGAAGAAGAG CTCAAAGTCC CTGGCTCATG CAGGAGTGGC CTTGGCCAAA 720

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Cont

CCCCTCCCCA GGACCCCTGA GCAGGAGAGC TGCACCATCC CAGTGCAGGA GGATGAGTCT 780
 CCACTCGGCG CCCCATATGT TAGAAACACC CCGCAGTTCA CCAAGCCTCT GAAGGAACCA 840
 GGCCTTGGGC AACTCTGTTT TAAGCAGCTT GGCGAGGGCC TACGGCCGGC TCTGCCTCGA 900
 TCAGAACTCC ACAAACATGAT CAGCCCCTTG CAATGTCTGA ACCACGTGTG GAAACTGCAC 960
 CACCCCCAGG ACGGAGGCCC CCTGCCCCCTG CCCACGCACC CCTTCCCCTA TAGCAGACTG 1020
 CCTCATCCCT TCCCATTCCA CCCTCTCCAG CCCTGGAAAC CTCACCCTCT GGAGTCCTTC 1080
 CTGGGCAAAC TGGCCTGTGT AGACAGCCAG AAACCCTTGC CTGACCCACA CCTGAGCAAA 1140
 CTGGCCTGTG TAGACAGTCC AAAGCCCCTG CCTGGCCCAC ACCTGGAGCC CAGCTGCCTG 1200
 TCTCGTGGTG CCCATGAGAA GTTTTCTGTG GAGGAATACC TAGTGCATGC TCTGCAAGGC 1260
 AGCGTGAGCT CAAGCCAGGC CCACAGCCTG ACCAGCCTGG CCAAGACCTG GGCAGCACGG 1320
 GGCTCCAGAT CCCGGGAGCC CAGCCCCAAA ACTGAGGACA ACGAGGGTGT CCTGCTCACT 1380
 GAGAACTCA AGCCAGTGGA TTATGAGTAC CGAGAAGAAG TCCACTGGGC CACGCACCAG 1440
 CTCCGCCTGG GCAGAGGCTC CTTCGGAGAG GTGCACAGGA TGGAGGACAA GCAGACTGGC 1500
 TTCCAGTGCG CTGTCAAAAA GGTGCGCCTG GAAGTATTTT GGGCAGAGGA GCTGATGGCA 1560
 TGTGCAGGAT TGACCTCACC CAGAATTGTC CCTTTGTATG GAGCTGTGAG AGAAGGGCCT 1620
 TGGGTCAACA TCTTCATGGA GCTGCTGGAA GGTGGCTCCC TGGGCCAGCT GGTCAAGGAG 1680
 CAGGGCTGTC TCCCAGAGGA CCGGGCCCTG TACTACCTGG GCCAGGCCCT GGAGGGTCTG 1740
 GAATACCTCC ACTCACGAAG GATTCTGCAT GGGGACGTCA AAGCTGACAA CGTGCTCCTG 1800
 TCCAGCGATG GGAGCCACGC AGCCCTCTGT GACTTTGGCC ATGCTGTGTG TCTTCAACCT 1860
 GATGGCCTGG GAAAGTCCTT GCTCACAGGG GACTACATCC CTGGCACAGA GACCCACATG 1920
 GCTCCGGAGG TGGTGCTGGG CAGGAGCTGC GACGCCAAGG TGGATGTCTG GAGCAGCTGC 1980
 TGTATGATGC TGCACATGCT CAACGGCTGC CACCCTGGA CTCAGTTCTT CCGAGGGCCG 2040
 CTCTGCCTCA AGATTGCCAG CGAGCCTCCG CCTGTGAGGG AGATCCCACC CTCCTGCGCC 2100
 CCTCTCACAG CCCAGGCCAT CCAAGAGGGG CTGAGGAAAG AGCCCATCCA CCGCGTGTCT 2160
 GCAGCGGAGC TGGGAGGGAA GGTGAACCGG GCACTACAGC AAGTGGGAGG TCTGAAGAGC 2220
 CCTTGGAGGG GAGAATATAA AGAACCAAGA CATCCACCGC CAAATCAAGC CAATTACCAC 2280
 CAGACCCTCC ATGCCAGGCC GAGAGAGCTT TCGCCAAGGG CCCCAGGGCC CCGGCCAGCT 2340
 GAGGAGACAA CAGGCAGAGC CCCTAAGCTC CAGCCTCCTC TCCCACCAGA GCCCCAGAG 2400
 CCAAACAAGT CTCCTCCCTT GACTTTGAGC AAGGAGGAGT CTGGGATGTG GGAACCCTTA 2460
 CCTCTGTCTT CCCTGGAGCC AGCCCCTGCC AGAAACCCCA GCTCACCAGA GCGGAAAGCA 2520
 ACCGTCCCGG AGCAGGAACT GCAGCAGCTG GAAATAGAAT TATTCCTCAA CAGCCTGTCC 2580
 CAGCCATTTT CTCTGGAGGA GCAGGAGCAA ATTCTCTCGT GCCTCAGCAT CGACAGCCTC 2640
 TCCCTGTCTG ATGACAGTGA GAAGAACCCA TCAAAGGCCT CTCAAAGCTC GCGGGACACC 2700
 CTGAGCTCAG GCGTACACTC CTGGAGCAGC CAGGCCGAGG CTCGAAGCTC CAGCTGGAAC 2760

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ATGGTGCTGG	CCCGGGGGCG	GCCCACCGAC	ACCCCAAGCT	ATTTCAATGG	TGTGAAAGTC	2820
CAAATACAGT	CTCTTAATGG	TGAACACCTG	CACATCCGGG	AGTTCCACCG	GGTCAAAGTG	2880
GGAGACATCG	CCACTGGCAT	CAGCAGCCAG	ATCCCAGCTG	CAGCCTTCAG	CTTGGTCAAC	2940
AAAGACGGGC	AGCCTGTTCG	CTACGACATG	GAGGTGCCAG	ACTCGGGCAT	CGACCTGCAG	3000
TGCACACTGG	CCCCTGATGG	CAGCTTCGCC	TGGAGCTGGA	GGGTCAAGCA	TGGCCAGCTG	3060
GAGAACAGGC	CCTAACCCTG	CCCTCCACCG	CCGGCTCCAC	ACTGCCGGAA	AGCAGCCTTC	3120
CTGCTCGGTG	CACGATGCTG	CCCTGAAAAC	ACAGGCTCAG	CCGTTCCCAG	GGGATTGCCA	3180
GCCCCCGGC	TCACAGTGGG	AACCAGGGCC	TCGCAGCAGC	AAGGTGGGGG	CAAGCAGAAT	3240
GCCTCCCAGG	ATTTACACAC	TGAGCCCTGC	CCCACCCTGC	TGAAAAACA	TCCGCCACGT	3300
GAAGAGACAG	AAGGAGGATG	GCAGGAGTTA	CCTGGGGAAA	CAAAACAGGG	ATCTTTTCT	3360
GCCCCTGCTC	CAGTCGAGTT	GGCCTGACCC	GCTTGATCA	GTGACCATT	GTTGGCAGAC	3420
AGGGGAGAGC	AGCTTCCAGC	CTGGGTCAGA	AGGGGTGGGC	GAGCCCTTCG	GCCCCTCACC	3480
CTCCAGGCTG	CTGTGAGAGT	GTCAAGTGTG	TAAGGGCCCA	AACTCAGGTT	CAGTGCAGAA	3540
CCAGGTCAGC	AGGTATGCCC	GCCCGTAGGT	TAAGGGGGCC	CTCTAAACCC	CTTGCCCTGGC	3600
CTCACCTGGC	CAGCTCACCC	CTTTTGGGTG	TAGGGGAAAA	GAATGCCTGA	CCCTGGGAAG	3660
GCTCCCTGGT	AGAATACACC	ACACTTTTCA	GGTTGTTGCA	ACACAGGTCC	TGAGTTGACC	3720
TCTGGTTCAG	CCAAGGACCA	AAGAAGGTGT	GTAAGTGAAG	TGGTTCTCAG	TCCCCAGACA	3780
TGTGCCCCTT	TGCTGCTGGC	TACCACTCTT	CCCCAGAGCA	GCAGGCCCCG	AGCCCCTTCA	3840
GGCCCAGCAC	TGCCCCAGAC	TCGCTGGCAC	TCAGTTCCCT	CATCTGTAAA	GGTGAAGGGT	3900
GATGCAGGAT	ATGCCTGACA	GGAACAGTCT	GTGGATGGAC	ATGATCAGTG	CTAAGGAAAG	3960
CAGCAGAGAG	AGACGTCCGG	CGCCCCAGCC	CCACTATCAG	TGTCCAGCGT	GCTGGTTCCC	4020
CAGAGCACAG	CTCAGCATCA	CACTGACACT	CACCCTGCCC	TGCCCCTGCC	CAGAGGGTAC	4080
TGCCGACGGC	ACTTTGCACT	CTGATGACCT	CAAAGCACTT	TCATGGCTGC	CCTCTGGCAG	4140
GGCAGGGCAG	GGCAGTGACA	CTGTAGGAGC	ATAGCAAGCC	AGGAGATGGG	GTGAAGGGAC	4200
ACAGTCTTGA	GCTGTCCACA	TGCATGTGAC	TCCTCAAACC	TCTTCCAGAT	TTCTCTAAGA	4260
ATAGCACCCC	CTTCCCCATT	GCCCCAGCTT	AGCCTCTTCT	CCCAGGGGAG	CTACTCAGGA	4320
CTCACGTAGC	ATTAAATCAG	CTGTGAATCG	TCAGGGGGTG	TCTGCTAGCC	TCAACCTCCT	4380
GGGGCAGGGG	ACGCCGAGAC	TCCGTGGGAG	AAGCTCATTC	CCACATCTTG	CCAAGACAGC	4440
CTTTGTCCAG	CTGTCCACAT	TGAGTCAGAC	TGCTCCCGGG	GAGAGAGCCC	CGGCCCCCAG	4500
CACATAAAGA	ACTGCAGCCT	TGGTACTGCA	GAGTCTGGGT	TGTAGAGAAC	TCTTTGTAAG	4560
CAATAAAGTT	TGGGGTGATG	ACAAATGTTA	AAAAAA			4596

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 947 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met	Ala	Val	Met	Glu	Met	Ala	Cys	Pro	Gly	Ala	Pro	Gly	Ser	Ala	Val	1	5	10	15
Gly	Gln	Gln	Lys	Glu	Leu	Pro	Lys	Pro	Lys	Glu	Lys	Thr	Pro	Pro	Leu	20	25	30	
Gly	Lys	Lys	Gln	Ser	Ser	Val	Tyr	Lys	Leu	Glu	Ala	Val	Glu	Lys	Ser	35	40	45	
Pro	Val	Phe	Cys	Gly	Lys	Trp	Glu	Ile	Leu	Asn	Asp	Val	Ile	Thr	Lys	50	55	60	
Gly	Thr	Ala	Lys	Glu	Gly	Ser	Glu	Ala	Gly	Pro	Ala	Ala	Ile	Ser	Ile	65	70	75	80
Ile	Ala	Gln	Ala	Glu	Cys	Glu	Asn	Ser	Gln	Glu	Phe	Ser	Pro	Thr	Phe	85	90	95	
Ser	Glu	Arg	Ile	Phe	Ile	Ala	Gly	Ser	Lys	Gln	Tyr	Ser	Gln	Ser	Glu	100	105	110	
Ser	Leu	Asp	Gln	Ile	Pro	Asn	Asn	Val	Ala	His	Ala	Thr	Glu	Gly	Lys	115	120	125	
Met	Ala	Arg	Val	Cys	Trp	Lys	Gly	Lys	Arg	Arg	Ser	Lys	Ala	Arg	Lys	130	135	140	
Lys	Arg	Lys	Lys	Lys	Ser	Ser	Lys	Ser	Leu	Ala	His	Ala	Gly	Val	Ala	145	150	155	160
Leu	Ala	Lys	Pro	Leu	Pro	Arg	Thr	Pro	Glu	Gln	Glu	Ser	Cys	Thr	Ile	165	170	175	
Pro	Val	Gln	Glu	Asp	Glu	Ser	Pro	Leu	Gly	Ala	Pro	Tyr	Val	Arg	Asn	180	185	190	
Thr	Pro	Gln	Phe	Thr	Lys	Pro	Leu	Lys	Glu	Pro	Gly	Leu	Gly	Gln	Leu	195	200	205	
Cys	Phe	Lys	Gln	Leu	Gly	Glu	Gly	Leu	Arg	Pro	Ala	Leu	Pro	Arg	Ser	210	215	220	
Glu	Leu	His	Lys	Leu	Ile	Ser	Pro	Leu	Gln	Cys	Leu	Asn	His	Val	Trp	225	230	235	240
Lys	Leu	His	His	Pro	Gln	Asp	Gly	Gly	Pro	Leu	Pro	Leu	Pro	Thr	His	245	250	255	
Pro	Phe	Pro	Tyr	Ser	Arg	Leu	Pro	His	Pro	Phe	Pro	Phe	His	Pro	Leu	260	265	270	
Gln	Pro	Trp	Lys	Pro	His	Pro	Leu	Glu	Ser	Phe	Leu	Gly	Lys	Leu	Ala	275	280	285	
Cys	Val	Asp	Ser	Gln	Lys	Pro	Leu	Pro	Asp	Pro	His	Leu	Ser	Lys	Leu	290	295	300	
Ala	Cys	Val	Asp	Ser	Pro	Lys	Pro	Leu	Pro	Gly	Pro	His	Leu	Glu	Pro	305	310	315	320

Ser Cys Leu Ser Arg Gly Ala His Glu Lys Phe Ser Val Glu Glu Tyr
 325 330 335
 Leu Val His Ala Leu Gln Gly Ser Val Ser Ser Ser Gln Ala His Ser
 340 345 350
 Leu Thr Ser Leu Ala Lys Thr Trp Ala Ala Arg Gly Ser Arg Ser Arg
 355 360 365
 Glu Pro Ser Pro Lys Thr Glu Asp Asn Glu Gly Val Leu Leu Thr Glu
 370 375 380
 Lys Leu Lys Pro Val Asp Tyr Glu Tyr Arg Glu Glu Val His Trp Ala
 385 390 395 400
 Thr His Gln Leu Arg Leu Gly Arg Gly Ser Phe Gly Glu Val His Arg
 405 410 415
 Met Glu Asp Lys Gln Thr Gly Phe Gln Cys Ala Val Lys Lys Val Arg
 420 425 430
 Leu Glu Val Phe Arg Ala Glu Glu Leu Met Ala Cys Ala Gly Leu Thr
 435 440 445
 Ser Pro Arg Ile Val Pro Leu Tyr Gly Ala Val Arg Glu Gly Pro Trp
 450 455 460
 Val Asn Ile Phe Met Glu Leu Leu Glu Gly Gly Ser Leu Gly Gln Leu
 465 470 475 480
 Val Lys Glu Gln Gly Cys Leu Pro Glu Asp Arg Ala Leu Tyr Tyr Leu
 485 490 495
 Gly Gln Ala Leu Glu Gly Leu Glu Tyr Leu His Ser Arg Arg Ile Leu
 500 505 510
 His Gly Asp Val Lys Ala Asp Asn Val Leu Leu Ser Ser Asp Gly Ser
 515 520 525
 His Ala Ala Leu Cys Asp Phe Gly His Ala Val Cys Leu Gln Pro Asp
 530 535 540
 Gly Leu Gly Lys Ser Leu Leu Thr Gly Asp Tyr Ile Pro Gly Thr Glu
 545 550 555 560
 Thr His Met Ala Pro Glu Val Val Leu Gly Arg Ser Cys Asp Ala Lys
 565 570 575
 Val Asp Val Trp Ser Ser Cys Cys Met Met Leu His Met Leu Asn Gly
 580 585 590
 Cys His Pro Trp Thr Gln Phe Phe Arg Gly Pro Leu Cys Leu Lys Ile
 595 600 605
 Ala Ser Glu Pro Pro Pro Val Arg Glu Ile Pro Pro Ser Cys Ala Pro
 610 615 620
 Leu Thr Ala Gln Ala Ile Gln Glu Gly Leu Arg Lys Glu Pro Ile His
 625 630 635 640
 Arg Val Ser Ala Ala Glu Leu Gly Gly Lys Val Asn Arg Ala Leu Gln
 645 650 655
 Gln Val Gly Gly Leu Lys Ser Pro Trp Arg Gly Glu Tyr Lys Glu Pro
 660 665 670
 Arg His Pro Pro Pro Asn Gln Ala Asn Tyr His Gln Thr Leu His Ala

675					680					685					
Gln	Pro	Arg	Glu	Leu	Ser	Pro	Arg	Ala	Pro	Gly	Pro	Arg	Pro	Ala	Glu
690						695					700				
Glu	Thr	Thr	Gly	Arg	Ala	Pro	Lys	Leu	Gln	Pro	Pro	Leu	Pro	Pro	Glu
705					710					715					720
Pro	Pro	Glu	Pro	Asn	Lys	Ser	Pro	Pro	Leu	Thr	Leu	Ser	Lys	Glu	Glu
				725					730					735	
Ser	Gly	Met	Trp	Glu	Pro	Leu	Pro	Leu	Ser	Ser	Leu	Glu	Pro	Ala	Pro
			740					745					750		
Ala	Arg	Asn	Pro	Ser	Ser	Pro	Glu	Arg	Lys	Ala	Thr	Val	Pro	Glu	Gln
		755					760					765			
Glu	Leu	Gln	Gln	Leu	Glu	Ile	Glu	Leu	Phe	Leu	Asn	Ser	Leu	Ser	Gln
	770					775					780				
Pro	Phe	Ser	Leu	Glu	Glu	Gln	Glu	Gln	Ile	Leu	Ser	Cys	Leu	Ser	Ile
785						790					795				800
Asp	Ser	Leu	Ser	Leu	Ser	Asp	Asp	Ser	Glu	Lys	Asn	Pro	Ser	Lys	Ala
				805					810					815	
Ser	Gln	Ser	Ser	Arg	Asp	Thr	Leu	Ser	Ser	Gly	Val	His	Ser	Trp	Ser
			820					825					830		
Ser	Gln	Ala	Glu	Ala	Arg	Ser	Ser	Ser	Trp	Asn	Met	Val	Leu	Ala	Arg
		835					840					845			
Gly	Arg	Pro	Thr	Asp	Thr	Pro	Ser	Tyr	Phe	Asn	Gly	Val	Lys	Val	Gln
	850					855					860				
Ile	Gln	Ser	Leu	Asn	Gly	Glu	His	Leu	His	Ile	Arg	Glu	Phe	His	Arg
865						870					875				880
Val	Lys	Val	Gly	Asp	Ile	Ala	Thr	Gly	Ile	Ser	Ser	Gln	Ile	Pro	Ala
				885					890					895	
Ala	Ala	Phe	Ser	Leu	Val	Thr	Lys	Asp	Gly	Gln	Pro	Val	Arg	Tyr	Asp
			900					905					910		
Met	Glu	Val	Pro	Asp	Ser	Gly	Ile	Asp	Leu	Gln	Cys	Thr	Leu	Ala	Pro
		915					920					925			
Asp	Gly	Ser	Phe	Ala	Trp	Ser	Trp	Arg	Val	Lys	His	Gly	Gln	Leu	Glu
	930					935					940				
Asn	Arg	Pro													
945															

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CAGGATCCTC ATGGCTGCAG CTAGCGTGAC

30

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide PCR primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGTCGACTTA GAGCCCTGTC AGGTCCACAA TG

32

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide probe"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATGCCATTG GGGATTTTCCT CTTT

24

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide probe"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CAGTAAAGAG GAAATCCCCA ATGG

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Glu	Tyr	Met	Ser	Thr	Gly	Ser	Asp	Glu	Lys	Glu	Glu	Ile	Asp	Leu
1				5					10					15	

Leu	Ile	Asn	His	Leu	Asn	Val	Ser	Glu	Val	Leu	Asp	Ile	Met	Glu	Asn	
			20					25					30			
Leu	Tyr	Ala	Ser	Glu	Glu	Pro	Ala	Val	Tyr	Glu	Pro	Ser	Leu	Met	Thr	
		35					40					45				
Met	Cys	Pro	Asp	Ser	Asn	Gln	Asn	Lys	Glu	His	Ser	Glu	Ser	Leu	Leu	
	50					55					60					
Arg	Ser	Gly	Gln	Glu	Val	Pro	Trp	Leu	Ser	Ser	Val	Arg	Tyr	Gly	Thr	
65					70					75					80	
Val	Glu	Asp	Leu	Leu	Ala	Phe	Ala	Asn	His	Ile	Ser	Asn	Thr	Thr	Lys	
			85						90					95		
His	Phe	Tyr	Arg	Cys	Arg	Pro	Gln	Glu	Ser	Gly	Ile	Leu	Leu	Asn	Met	
			100					105					110			
Val	Ile	Ser	Pro	Gln	Asn	Gly	Arg	Tyr	Gln	Ile	Asp	Ser	Asp	Val	Leu	
		115					120					125				
Leu	Val	Pro	Trp	Lys	Leu	Thr	Tyr	Arg	Ser	Ile	Gly	Ser	Gly	Phe	Val	
	130					135					140					
Pro	Arg	Gly	Ala	Phe	Gly	Lys	Val	Tyr	Leu	Ala	Gln	Asp	Met	Lys	Thr	
145					150					155					160	
Lys	Lys	Arg	Met	Ala	Cys	Lys	Leu	Ile	Pro	Val	Asp	Gln	Phe	Lys	Pro	
				165					170					175		
Ser	Asp	Val	Glu	Ile	Gln	Ala	Cys	Phe	Arg	His	Glu	Asn	Ile	Ala	Glu	
		180						185					190			
Leu	Tyr	Gly	Ala	Val	Leu	Trp	Gly	Asp	Thr	Val	His	Leu	Phe	Met	Glu	
	195						200					205				
Ala	Gly	Glu	Gly	Gly	Ser	Val	Leu	Glu	Lys	Leu	Glu	Ser	Cys	Gly	Pro	
	210					215					220					
Met	Arg	Glu	Phe	Glu	Ile	Ile	Trp	Val	Thr	Lys	His	Val	Leu	Lys	Gly	
225					230					235					240	
Leu	Asp	Phe	Leu	His	Ser	Lys	Lys	Val	Ile	His	His	Asp	Ile	Lys	Pro	
			245						250					255		
Ser	Asn	Ile	Val	Phe	Met	Ser	Thr	Lys	Ala	Val	Leu	Val	Asp	Phe	Gly	
		260						265					270			
Leu	Ser	Val	Gln	Met	Thr	Glu	Asp	Val	Tyr	Leu	Pro	Lys	Asp	Leu	Arg	
		275					280					285				
Gly	Thr	Glu	Ile	Tyr	Met	Ser	Pro	Glu	Val	Ile	Leu	Cys	Arg	Gly	His	
	290					295					300					
Ser	Thr	Lys	Ala	Asp	Ile	Tyr	Ser	Leu	Gly	Ala	Thr	Leu	Ile	His	Met	
305					310					315					320	
Gln	Thr	Gly	Thr	Pro	Pro	Trp	Val	Lys	Arg	Tyr	Pro	Arg	Ser	Ala	Tyr	
			325						330					335		
Pro	Ser	Tyr	Leu	Tyr	Ile	Ile	His	Lys	Gln	Ala	Pro	Pro	Leu	Glu	Asp	
			340					345					350			
Ile	Ala	Gly	Asp	Cys	Ser	Pro	Gly	Met	Arg	Glu	Leu	Ile	Glu	Ala	Ala	
		355					360					365				

Leu Glu Arg Asn Pro Asn His Arg Pro Lys Ala Ala Asp Leu Leu Lys
 370 375 380
 His Glu Ala Leu Asn Pro Pro Arg Glu Asp Gln Pro Arg Cys Gln Ser
 385 390 395 400
 Leu Asp Ser Ala Leu Phe Asp Arg Lys Arg Leu Leu Ser Arg Lys Glu
 405 410 415
 Leu Glu Leu Pro Glu Asn Ile Ala Asp Ser Ser Cys Thr Gly Ser Thr
 420 425 430
 Glu Glu Ser Glu Val Leu Arg Arg Gln Arg Ser Leu Tyr Ile Asp Leu
 435 440 445
 Gly Ala Leu Ala Gly Tyr Phe Asn Ile Val Arg Gly Pro Pro Thr Leu
 450 455 460
 Glu Tyr Gly
 465

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Glu Tyr Met Ser Thr Gly Ser Asp Asn Lys Glu Glu Ile Asp Leu
 1 5 10 15
 Leu Ile Lys His Leu Asn Val Ser Asp Val Ile Asp Ile Met Glu Asn
 20 25 30
 Leu Tyr Ala Ser Glu Glu Pro Ala Val Tyr Glu Pro Ser Leu Met Thr
 35 40 45
 Met Cys Gln Asp Ser Asn Gln Asn Asp Glu Arg Ser Lys Ser Leu Leu
 50 55 60
 Leu Ser Gly Gln Glu Val Pro Trp Leu Ser Ser Val Arg Tyr Gly Thr
 65 70 75 80
 Val Glu Asp Leu Leu Ala Phe Ala Asn His Ile Ser Asn Thr Ala Lys
 85 90 95
 His Phe Tyr Gly Gln Arg Pro Gln Glu Ser Gly Ile Leu Leu Asn Met
 100 105 110
 Val Ile Thr Pro Gln Asn Gly Arg Tyr Gln Ile Asp Ser Asp Val Leu
 115 120 125
 Leu Ile Pro Trp Lys Leu Thr Tyr Arg Asn Ile Gly Ser Asp Phe Ile
 130 135 140
 Pro Arg Gly Ala Phe Gly Lys Val Tyr Leu Ala Gln Asp Ile Lys Thr
 145 150 155 160
 Lys Lys Arg Met Ala Cys Lys Leu Ile Pro Val Asp Gln Phe Lys Pro
 165 170 175
 Ser Asp Val Glu Ile Gln Ala Cys Phe Arg His Glu Asn Ile Ala Glu

180					185					190					
Leu	Tyr	Gly	Ala	Val	Leu	Trp	Gly	Glu	Thr	Val	His	Leu	Phe	Met	Glu
		195					200					205			
Ala	Gly	Glu	Gly	Gly	Ser	Val	Leu	Glu	Lys	Leu	Glu	Ser	Cys	Gly	Pro
	210					215					220				
Met	Arg	Glu	Phe	Glu	Ile	Ile	Trp	Val	Thr	Lys	His	Val	Leu	Lys	Gly
	225					230					235				240
Leu	Asp	Phe	Leu	His	Ser	Lys	Lys	Val	Ile	His	His	Asp	Ile	Lys	Pro
				245					250					255	
Ser	Asn	Ile	Val	Phe	Met	Ser	Thr	Lys	Ala	Val	Leu	Val	Asp	Phe	Gly
			260					265					270		
Leu	Ser	Val	Gln	Met	Thr	Glu	Asp	Val	Tyr	Pro	Phe	Lys	Asp	Leu	Arg
		275					280					285			
Gly	Thr	Glu	Ile	Tyr	Met	Ser	Pro	Glu	Val	Ile	Leu	Cys	Arg	Gly	His
	290					295					300				
Ser	Thr	Lys	Ala	Asp	Ile	Tyr	Ser	Leu	Gly	Ala	Thr	Leu	Ile	His	Met
	305					310					315				320
Gln	Thr	Gly	Thr	Pro	Pro	Trp	Val	Lys	Arg	Tyr	Pro	Arg	Ser	Ala	Tyr
				325					330					335	
Pro	Ser	Tyr	Leu	Tyr	Ile	Ile	His	Lys	Gln	Ala	Pro	Pro	Leu	Glu	Asp
			340					345					350		
Ile	Ala	Asp	Asp	Cys	Ser	Pro	Gly	Met	Arg	Glu	Leu	Ile	Glu	Ala	Ser
		355					360					365			
Leu	Glu	Arg	Asn	Pro	Asn	His	Arg	Pro	Arg	Ala	Ala	Asp	Leu	Leu	Lys
	370					375					380				
His	Glu	Ala	Leu	Asn	Pro	Pro	Arg	Glu	Asp	Gln	Pro	Arg	Cys	Gln	Ser
	385					390					395				400
Leu	Asp	Ser	Ala	Leu	Leu	Glu	Arg	Lys	Arg	Leu	Leu	Ser	Arg	Lys	Glu
				405					410					415	
Leu	Glu	Leu	Pro	Glu	Asn	Ile	Ala	Asp	Ser	Ser	Cys	Thr	Gly	Ser	Thr
			420					425					430		
Glu	Glu	Ser	Glu	Met	Leu	Lys	Arg	Gln	Arg	Ser	Leu	Tyr	Ile	Asp	Leu
		435					440					445			
Gly	Ala	Leu	Ala	Gly	Tyr	Phe	Asn	Leu	Val	Arg	Gly	Pro	Pro	Thr	Leu
	450					455					460				
Glu	Tyr	Gly													
	465														

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 947 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Val	Met	Glu	Met	Ala	Cys	Pro	Gly	Ala	Pro	Gly	Ser	Ala	Val	1	5	10	15
Gly	Gln	Gln	Lys	Glu	Leu	Pro	Lys	Pro	Lys	Glu	Lys	Thr	Pro	Pro	Leu	20	25	30	
Gly	Lys	Lys	Gln	Ser	Ser	Val	Tyr	Lys	Leu	Glu	Ala	Val	Glu	Lys	Ser	35	40	45	
Pro	Val	Phe	Cys	Gly	Lys	Trp	Glu	Ile	Leu	Asn	Asp	Val	Ile	Thr	Lys	50	55	60	
Gly	Thr	Ala	Lys	Glu	Gly	Ser	Glu	Ala	Gly	Pro	Ala	Ala	Ile	Ser	Ile	65	70	75	80
Ile	Ala	Gln	Ala	Glu	Cys	Glu	Asn	Ser	Gln	Glu	Phe	Ser	Pro	Thr	Phe	85	90	95	
Ser	Glu	Arg	Ile	Phe	Ile	Ala	Gly	Ser	Lys	Gln	Tyr	Ser	Gln	Ser	Glu	100	105	110	
Ser	Leu	Asp	Gln	Ile	Pro	Asn	Asn	Val	Ala	His	Ala	Thr	Glu	Gly	Lys	115	120	125	
Met	Ala	Arg	Val	Cys	Trp	Lys	Gly	Lys	Arg	Arg	Ser	Lys	Ala	Arg	Lys	130	135	140	
Lys	Arg	Lys	Lys	Lys	Ser	Ser	Lys	Ser	Leu	Ala	His	Ala	Gly	Val	Ala	145	150	155	160
Leu	Ala	Lys	Pro	Leu	Pro	Arg	Thr	Pro	Glu	Gln	Glu	Ser	Cys	Thr	Ile	165	170	175	
Pro	Val	Gln	Glu	Asp	Glu	Ser	Pro	Leu	Gly	Ala	Pro	Tyr	Val	Arg	Asn	180	185	190	
Thr	Pro	Gln	Phe	Thr	Lys	Pro	Leu	Lys	Glu	Pro	Gly	Leu	Gly	Gln	Leu	195	200	205	
Cys	Phe	Lys	Gln	Leu	Gly	Glu	Gly	Leu	Arg	Pro	Ala	Leu	Pro	Arg	Ser	210	215	220	
Glu	Leu	His	Lys	Leu	Ile	Ser	Pro	Leu	Gln	Cys	Leu	Asn	His	Val	Trp	225	230	235	240
Lys	Leu	His	His	Pro	Gln	Asp	Gly	Gly	Pro	Leu	Pro	Leu	Pro	Thr	His	245	250	255	
Pro	Phe	Pro	Tyr	Ser	Arg	Leu	Pro	His	Pro	Phe	Pro	Phe	His	Pro	Leu	260	265	270	
Gln	Pro	Trp	Lys	Pro	His	Pro	Leu	Glu	Ser	Phe	Leu	Gly	Lys	Leu	Ala	275	280	285	
Cys	Val	Asp	Ser	Gln	Lys	Pro	Leu	Pro	Asp	Pro	His	Leu	Ser	Lys	Leu	290	295	300	
Ala	Cys	Val	Asp	Ser	Pro	Lys	Pro	Leu	Pro	Gly	Pro	His	Leu	Glu	Pro	305	310	315	320
Ser	Cys	Leu	Ser	Arg	Gly	Ala	His	Glu	Lys	Phe	Ser	Val	Glu	Glu	Tyr	325	330	335	
Leu	Val	His	Ala	Leu	Gln	Gly	Ser	Val	Ser	Ser	Ser	Gln	Ala	His	Ser	340	345	350	

Leu	Thr	Ser	Leu	Ala	Lys	Thr	Trp	Ala	Ala	Arg	Gly	Ser	Arg	Ser	Arg		
		355					360					365					
Glu	Pro	Ser	Pro	Lys	Thr	Glu	Asp	Asn	Glu	Gly	Val	Leu	Leu	Thr	Glu		
	370					375					380						
Lys	Leu	Lys	Pro	Val	Asp	Tyr	Glu	Tyr	Arg	Glu	Glu	Val	His	Trp	Ala		
385					390					395					400		
Thr	His	Gln	Leu	Arg	Leu	Gly	Arg	Gly	Ser	Phe	Gly	Glu	Val	His	Arg		
			405						410					415			
Met	Glu	Asp	Lys	Gln	Thr	Gly	Phe	Gln	Cys	Ala	Val	Lys	Lys	Val	Arg		
			420					425					430				
Leu	Glu	Val	Phe	Arg	Ala	Glu	Glu	Leu	Met	Ala	Cys	Ala	Gly	Leu	Thr		
		435					440					445					
Ser	Pro	Arg	Ile	Val	Pro	Leu	Tyr	Gly	Ala	Val	Arg	Glu	Gly	Pro	Trp		
	450					455					460						
Val	Asn	Ile	Phe	Met	Glu	Leu	Leu	Glu	Gly	Gly	Ser	Leu	Gly	Gln	Leu		
465					470					475					480		
Val	Lys	Glu	Gln	Gly	Cys	Leu	Pro	Glu	Asp	Arg	Ala	Leu	Tyr	Tyr	Leu		
			485						490					495			
Gly	Gln	Ala	Leu	Glu	Gly	Leu	Glu	Tyr	Leu	His	Ser	Arg	Arg	Ile	Leu		
			500					505					510				
His	Gly	Asp	Val	Lys	Ala	Asp	Asn	Val	Leu	Leu	Ser	Ser	Asp	Gly	Ser		
		515					520					525					
His	Ala	Ala	Leu	Cys	Asp	Phe	Gly	His	Ala	Val	Cys	Leu	Gln	Pro	Asp		
	530					535					540						
Gly	Leu	Gly	Lys	Ser	Leu	Leu	Thr	Gly	Asp	Tyr	Ile	Pro	Gly	Thr	Glu		
545					550				555						560		
Thr	His	Met	Ala	Pro	Glu	Val	Val	Leu	Gly	Arg	Ser	Cys	Asp	Ala	Lys		
			565						570					575			
Val	Asp	Val	Trp	Ser	Ser	Cys	Cys	Met	Met	Leu	His	Met	Leu	Asn	Gly		
			580					585					590				
Cys	His	Pro	Trp	Thr	Gln	Phe	Phe	Arg	Gly	Pro	Leu	Cys	Leu	Lys	Ile		
		595				600					605						
Ala	Ser	Glu	Pro	Pro	Pro	Val	Arg	Glu	Ile	Pro	Pro	Ser	Cys	Ala	Pro		
	610					615					620						
Leu	Thr	Ala	Gln	Ala	Ile	Gln	Glu	Gly	Leu	Arg	Lys	Glu	Pro	Ile	His		
625					630					635					640		
Arg	Val	Ser	Ala	Ala	Glu	Leu	Gly	Gly	Lys	Val	Asn	Arg	Ala	Leu	Gln		
			645						650					655			
Gln	Val	Gly	Gly	Leu	Lys	Ser	Pro	Trp	Arg	Gly	Glu	Tyr	Lys	Glu	Pro		
			660					665					670				
Arg	His	Pro	Pro	Pro	Asn	Gln	Ala	Asn	Tyr	His	Gln	Thr	Leu	His	Ala		
		675				680						685					
Gln	Pro	Arg	Glu	Leu	Ser	Pro	Arg	Ala	Pro	Gly	Pro	Arg	Pro	Ala	Glu		
	690					695					700						
Glu	Thr	Thr	Gly	Arg	Ala	Pro	Lys	Leu	Gln	Pro	Pro	Leu	Pro	Pro	Glu		

705		710		715		720									
Pro	Pro	Glu	Pro	Asn	Lys	Ser	Pro	Pro	Leu	Thr	Leu	Ser	Lys	Glu	Glu
				725					730					735	
Ser	Gly	Met	Trp	Glu	Pro	Leu	Pro	Leu	Ser	Ser	Leu	Glu	Pro	Ala	Pro
			740					745					750		
Ala	Arg	Asn	Pro	Ser	Ser	Pro	Glu	Arg	Lys	Ala	Thr	Val	Pro	Glu	Gln
		755					760					765			
Glu	Leu	Gln	Gln	Leu	Glu	Ile	Glu	Leu	Phe	Leu	Asn	Ser	Leu	Ser	Gln
	770					775					780				
Pro	Phe	Ser	Leu	Glu	Glu	Gln	Glu	Gln	Ile	Leu	Ser	Cys	Leu	Ser	Ile
	785				790					795					800
Asp	Ser	Leu	Ser	Leu	Ser	Asp	Asp	Ser	Glu	Lys	Asn	Pro	Ser	Lys	Ala
				805					810					815	
Ser	Gln	Ser	Ser	Arg	Asp	Thr	Leu	Ser	Ser	Gly	Val	His	Ser	Trp	Ser
			820					825					830		
Ser	Gln	Ala	Glu	Ala	Arg	Ser	Ser	Ser	Trp	Asn	Met	Val	Leu	Ala	Arg
		835					840					845			
Gly	Arg	Pro	Thr	Asp	Thr	Pro	Ser	Tyr	Phe	Asn	Gly	Val	Lys	Val	Gln
	850					855					860				
Ile	Gln	Ser	Leu	Asn	Gly	Glu	His	Leu	His	Ile	Arg	Glu	Phe	His	Arg
	865				870					875					880
Val	Lys	Val	Gly	Asp	Ile	Ala	Thr	Gly	Ile	Ser	Ser	Gln	Ile	Pro	Ala
				885					890					895	
Ala	Ala	Phe	Ser	Leu	Val	Thr	Lys	Asp	Gly	Gln	Pro	Val	Arg	Tyr	Asp
			900					905					910		
Met	Glu	Val	Pro	Asp	Ser	Gly	Ile	Asp	Leu	Gln	Cys	Thr	Leu	Ala	Pro
		915					920					925			
Asp	Gly	Ser	Phe	Ala	Trp	Ser	Trp	Arg	Val	Lys	His	Gly	Gln	Leu	Glu
	930					935					940				
Asn	Arg	Pro													
	945														

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 688 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr	Leu	Thr	His	Thr	Thr	Ser	Leu	Phe	Ala	Pro	Pro	Asn	Leu	Ser	Pro
1				5					10					15	
Met	Gln	Asp	Phe	Ile	Gly	Ser	Val	Arg	Arg	Ser	Leu	Val	Phe	Lys	Gln
			20					25					30		
Ser	Gly	Asp	Phe	Asp	Thr	Gly	Ala	Ala	Gly	Val	Gly	Ser	Gly	Phe	Gly
		35					40					45			

Gly	Phe	Val	Glu	Lys	Leu	Gly	Ser	Ser	Ile	Arg	Lys	Ser	Ser	Ile	Gly
50						55					60				
Ile	Phe	Ser	Lys	Ala	His	Val	Pro	Ala	Leu	Pro	Ser	Ile	Ser	Lys	Ala
65					70					75					80
Glu	Leu	Pro	Ala	Lys	Ala	Arg	Lys	Asp	Asp	Thr	Pro	Pro	Ile	Arg	Trp
				85					90					95	
Arg	Lys	Gly	Glu	Met	Ile	Gly	Cys	Gly	Ala	Phe	Gly	Arg	Val	Tyr	Met
			100					105					110		
Gly	Met	Asn	Val	Asp	Ser	Gly	Glu	Leu	Leu	Ala	Ile	Lys	Glu	Val	Ser
		115					120					125			
Ile	Ala	Met	Asn	Gly	Ala	Ser	Arg	Glu	Arg	Ala	Gln	Ala	His	Val	Arg
	130					135					140				
Glu	Leu	Glu	Glu	Glu	Val	Asn	Leu	Leu	Lys	Asn	Leu	Ser	His	Pro	Asn
145					150					155					160
Ile	Val	Arg	Tyr	Leu	Gly	Thr	Ala	Arg	Glu	Ala	Gly	Ser	Leu	Asn	Ile
				165					170					175	
Leu	Leu	Glu	Phe	Val	Pro	Gly	Gly	Ser	Ile	Ser	Ser	Leu	Leu	Gly	Lys
			180					185					190		
Phe	Gly	Ser	Phe	Pro	Glu	Ser	Val	Ile	Arg	Met	Tyr	Thr	Lys	Gln	Leu
		195					200					205			
Leu	Leu	Gly	Leu	Glu	Tyr	Leu	His	Lys	Asn	Gly	Ile	Met	His	Arg	Asp
	210					215					220				
Ile	Lys	Gly	Ala	Asn	Ile	Leu	Val	Asp	Asn	Lys	Gly	Cys	Ile	Lys	Leu
225					230					235					240
Ala	Asp	Phe	Gly	Ala	Ser	Lys	Lys	Val	Val	Glu	Leu	Ala	Thr	Met	Thr
				245					250					255	
Gly	Ala	Lys	Ser	Met	Lys	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val
			260					265					270		
Ile	Leu	Gln	Thr	Gly	His	Ser	Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly
		275					280					285			
Cys	Thr	Ile	Ile	Glu	Met	Ala	Thr	Gly	Lys	Pro	Pro	Trp	Ser	Gln	Gln
	290					295					300				
Tyr	Gln	Glu	Val	Ala	Ala	Leu	Phe	His	Ile	Gly	Thr	Thr	Lys	Ser	His
305					310					315					320
Pro	Pro	Ile	Pro	Glu	His	Leu	Ser	Ala	Glu	Ser	Lys	Asp	Phe	Leu	Leu
				325					330					335	
Lys	Cys	Leu	Gln	Lys	Glu	Pro	His	Leu	Arg	His	Ser	Ala	Ser	Asn	Leu
			340					345					350		
Leu	Gln	His	Pro	Phe	Val	Thr	Ala	Glu	His	Gln	Glu	Ala	Arg	Pro	Phe
		355					360					365			
Leu	Arg	Ser	Ser	Phe	Met	Gly	Asn	Pro	Glu	Asn	Met	Ala	Ala	Gln	Arg
	370					375					380				
Met	Asp	Val	Arg	Thr	Ser	Ile	Ile	Pro	Asp	Met	Arg	Ala	Ser	Cys	Asn
385					390					395					400
Gly	Leu	Lys	Asp	Val	Cys	Gly	Val	Ser	Ala	Val	Arg	Cys	Ser	Thr	Val

405								410				415				
Tyr	Pro	Glu	Asn	Ser	Leu	Gly	Lys	Glu	Ser	Leu	Trp	Lys	Leu	Gly	Asn	
			420					425					430			
Ser	Asp	Asp	Asp	Met	Cys	Gln	Met	Asp	Asn	Asp	Asp	Phe	Met	Phe	Gly	
		435					440					445				
Ala	Ser	Val	Lys	Cys	Ser	Ser	Asp	Leu	His	Ser	Pro	Ala	Asn	Tyr	Lys	
		450				455					460					
Ser	Phe	Asn	Pro	Met	Cys	Glu	Pro	Asp	Asn	Asp	Trp	Pro	Cys	Lys	Phe	
465					470					475					480	
Asp	Glu	Ser	Pro	Glu	Leu	Thr	Lys	Ser	Gln	Ala	Asn	Leu	His	Tyr	Asp	
				485					490					495		
Gln	Ala	Thr	Ile	Lys	Pro	Thr	Asn	Asn	Pro	Ile	Met	Ser	Tyr	Lys	Glu	
			500					505					510			
Asp	Leu	Ala	Phe	Thr	Phe	Pro	Ser	Gly	Gln	Ser	Ala	Ala	Glu	Asp	Asp	
		515					520					525				
Asp	Glu	Leu	Thr	Glu	Ser	Lys	Ile	Arg	Ala	Phe	Leu	Asp	Glu	Lys	Ala	
		530				535					540					
Met	Asp	Leu	Lys	Lys	Leu	Gln	Thr	Pro	Leu	Tyr	Glu	Gly	Phe	Tyr	Asn	
545					550					555					560	
Ser	Leu	Asn	Val	Ser	Ser	Thr	Pro	Ser	Pro	Val	Gly	Thr	Gly	Asn	Lys	
				565				570						575		
Glu	Asn	Val	Pro	Ser	Asn	Ile	Asn	Leu	Pro	Pro	Lys	Ser	Arg	Ser	Pro	
			580					585					590			
Lys	Arg	Met	Leu	Ser	Arg	Arg	Leu	Ser	Thr	Ala	Ile	Glu	Gly	Ala	Cys	
		595					600					605				
Ala	Pro	Ser	Pro	Val	Thr	His	Ser	Lys	Arg	Ile	Ser	Asn	Ile	Gly	Gly	
		610				615					620					
Leu	Asn	Gly	Glu	Ala	Ile	Gln	Glu	Ala	Gln	Leu	Pro	Arg	His	Asn	Glu	
625					630					635					640	
Trp	Lys	Asp	Leu	Leu	Gly	Ser	Gln	Arg	Glu	Ala	Val	Asn	Ser	Ser	Phe	
				645					650					655		
Ser	Glu	Arg	Gln	Arg	Arg	Trp	Lys	Glu	Glu	Leu	Asp	Glu	Glu	Leu	Gln	
			660					665					670			
Arg	Lys	Arg	Glu	Ile	Met	Arg	Gln	Ala	Val	Asn	Leu	Ser	Pro	Pro	Lys	
			675				680					685				

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Tyr Tyr Thr Ser Lys Glu Val Ala Glu Trp Leu Lys Ser Ile

1	5	10	15
Gly Leu Glu Lys Tyr Ile Glu Gln Phe Ser Gln Asn Asn Ile Glu Gly	20	25	30
Arg His Leu Asn His Leu Thr Leu Pro Leu Leu Lys Asp Leu Gly Ile	35	40	45
Glu Asn Thr Ala Lys Gly Lys Gln Phe Leu Lys Gln Arg Asp Tyr Leu	50	55	60
Arg Glu Phe Pro Arg Pro Cys Ile Leu Arg Phe Ile Ala Cys Asn Gly	65	70	75
Gln Thr Arg Ala Val Gln Ser Arg Gly Asp Tyr Gln Lys Thr Leu Ala	85	90	95
Ile Ala Leu Lys Lys Phe Ser Leu Glu Asp Ala Ser Lys Phe Ile Val	100	105	110
Cys Val Ser Gln Ser Ser Arg Ile Lys Leu Ile Thr Glu Glu Glu Phe	115	120	125
Lys Gln Ile Cys Phe Asn Ser Ser Ser Pro Glu Arg Asp Arg Leu Ile	130	135	140
Ile Val Pro Lys Glu Lys Pro Cys Pro Ser Phe Glu Asp Leu Arg Arg	145	150	155
Ser Trp Glu Ile Glu Leu Ala Gln Pro Ala Ala Leu Ser Ser Gln Ser	165	170	175
Ser Leu Ser Pro Lys Leu Ser Ser Val Leu Pro Thr Ser Thr Gln Lys	180	185	190
Arg Ser Val Arg Ser Asn Asn Ala Lys Pro Phe Glu Ser Tyr Gln Arg	195	200	205
Pro Pro Ser Glu Leu Ile Asn Ser Arg Ile Ser Asp Phe Phe Pro Asp	210	215	220
His Gln Pro Lys Leu Leu Glu Lys Thr Ile Ser Asn Ser Leu Arg Arg	225	230	235
Asn Leu Ser Ile Arg Thr Ser Gln Gly His Asn Leu Gly Asn Phe Gly	245	250	255
Gln Glu Ile Leu Pro Arg Ser Ser Arg Arg Ala Arg Pro Ser Glu Leu	260	265	270
Val Cys Pro Leu Ser Ser Leu Arg Ile Ser Val Ala Glu Asp Val Asn	275	280	285
Arg Leu Pro Arg Ile Asp Arg Gly Phe Asp Pro Pro Leu Thr Val Ser	290	295	300
Ser Thr Gln Arg Ile Ser Arg Pro Pro Ser Leu Gln Lys Ser Ile Thr	305	310	315
Met Val Gly Val Glu Pro Leu Tyr Gln Ser Asn Gly Asn Glu Lys Ser	325	330	335
Ser Lys Tyr Asn Val Phe Ser Glu Ser Ala His Gly Asn His Gln Val	340	345	350
Leu Ser Phe Ser Pro Gly Ser Ser Pro Ser Phe Ile Glu Gln Pro Ser	355	360	365

Pro Ile Ser Pro Thr Ser Thr Thr Ser Glu Asp Thr Asn Thr Leu Glu
 370 375 380
 Glu Asp Thr Asp Asp Gln Ser Ile Lys Trp Ile Arg Gly Ala Leu Ile
 385 390 395 400
 Gly Ser Gly Ser Phe Gly Gln Val Tyr Leu Gly Met Asn Ala Ser Ser
 405 410 415
 Gly Glu Leu Met Ala Val Lys Gln Val Ile Leu Asp Ser Val Ser Glu
 420 425 430
 Ser Lys Asp Arg His Ala Lys Leu Leu Asp Ala Leu Ala Gly Glu Ile
 435 440 445
 Ala Leu Leu Gln Glu Leu Ser His Glu His Ile Val Gln Tyr Leu Gly
 450 455 460
 Ser Asn Leu Asn Ser Asp His Leu Asn Ile Phe Leu Glu Tyr Val Pro
 465 470 475 480
 Gly Gly Ser Val Ala Gly Leu Leu Thr Met Tyr Gly Ser Phe Glu Glu
 485 490 495
 Thr Leu Val Lys Asn Phe Ile Lys Gln Thr Leu Lys Gly Leu Glu Tyr
 500 505 510
 Leu His Ser Arg Gly Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile
 515 520 525
 Leu Val Asp Asn Lys Gly Lys Ile Lys Ile Ser Asp Phe Gly Ile Ser
 530 535 540
 Lys Lys Leu Glu Leu Asn Ser Thr Ser Thr Lys Thr Gly Gly Ala Arg
 545 550 555 560
 Pro Ser Phe Gln Gly Ser Ser Phe Trp Met Ala Pro Glu Val Val Lys
 565 570 575
 Gln Thr Met His Thr Glu Lys Thr Asp Ile Trp Ser Leu Gly Cys Leu
 580 585 590
 Val Ile Glu Met Leu Thr Ser Lys His Pro Tyr Pro Asn Cys Asp Gln
 595 600 605
 Met Gln Ala Ile Phe Arg Ile Gly Glu Asn Ile Leu Pro Glu Phe Pro
 610 615 620
 Ser Asn Ile Ser Ser Ser Ala Ile Asp Phe Leu Glu Lys Thr Phe Ala
 625 630 635 640
 Ile Asp Cys Asn Leu Arg Pro Thr Ala Ser Glu Leu Leu Ser His Pro
 645 650 655
 Phe Val Ser

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Glu Gln Thr Gln Thr Ala Glu Gly Thr Asp Leu Leu Ile Gly Asp
 1 5 10 15
 Glu Lys Thr Asn Asp Leu Pro Phe Val Gln Leu Phe Leu Glu Glu Ile
 20 25 30
 Gly Cys Thr Gln Tyr Leu Asp Ser Phe Ile Gln Cys Asn Leu Val Thr
 35 40 45
 Glu Glu Glu Ile Lys Tyr Leu Asp Lys Asp Ile Leu Ile Ala Leu Gly
 50 55 60
 Val Asn Lys Ile Gly Asp Arg Leu Lys Ile Leu Arg Lys Ser Lys Ser
 65 70 75 80
 Phe Gln Arg Asp Lys Arg Ile Glu Gln Val Asn Arg Leu Lys Asn Leu
 85 90 95
 Met Glu Lys Val Ser Ser Leu Ser Thr Ala Thr Leu Ser Met Asn Ser
 100 105 110
 Glu Leu Ile Pro Glu Lys His Cys Val Ile Phe Ile Leu Asn Asp Gly
 115 120 125
 Ser Ala Lys Lys Val Asn Val Asn Gly Cys Phe Asn Ala Asp Ser Ile
 130 135 140
 Lys Lys Arg Leu Ile Arg Arg Leu Pro His Glu Leu Leu Ala Thr Asn
 145 150 155 160
 Ser Asn Gly Glu Val Thr Lys Met Val Gln Asp Tyr Asp Val Phe Val
 165 170 175
 Leu Asp Tyr Thr Lys Asn Val Leu His Leu Leu Tyr Asp Val Glu Leu
 180 185 190
 Val Thr Ile Cys His Ala Asn Asp Arg Val Glu Lys Asn Arg Leu Ile
 195 200 205
 Phe Val Ser Lys Asp Gln Thr Pro Ser Asp Lys Ala Ile Ser Thr Ser
 210 215 220
 Lys Lys Leu Tyr Leu Arg Thr Leu Ser Ala Leu Ser Gln Val Gly Pro
 225 230 235 240
 Ser Ser Ser Asn Leu Leu Ala Gln Asn Lys Gly Ile Ser His Asn Asn
 245 250 255
 Ala Glu Gly Lys Leu Arg Ile Asp Asn Thr Glu Lys Asp Arg Ile Arg
 260 265 270
 Gln Ile Phe Asn Gln Arg Pro Pro Ser Glu Phe Ile Ser Thr Asn Leu
 275 280 285
 Ala Gly Tyr Phe Pro His Thr Asp Met Lys Arg Leu Gln Lys Thr Met
 290 295 300
 Arg Glu Ser Phe Arg His Ser Ala Arg Leu Ser Ile Ala Gln Arg Arg
 305 310 315 320
 Pro Leu Ser Ala Glu Ser Asn Asn Ile Gly Asp Ile Leu Leu Lys His
 325 330 335
 Ser Asn Ala Val Asp Met Ala Leu Leu Gln Gly Leu Asp Gln Thr Arg
 340 345 350

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Leu Ser Ser Lys Leu Asp Thr Thr Lys Ile Pro Lys Leu Ala His Lys
 355 360 365
 Arg Pro Glu Asp Asn Asp Ala Ile Ser Asn Gln Leu Glu Leu Leu Ser
 370 375 380
 Val Glu Ser Gly Glu Glu Glu Asp His Asp Phe Phe Gly Glu Asp Ser
 385 390 395 400
 Asp Ile Val Ser Leu Pro Thr Lys Ile Ala Thr Pro Lys Asn Trp Leu
 405 410 415
 Lys Gly Ala Cys Ile Gly Ser Gly Ser Phe Gly Ser Val Tyr Leu Gly
 420 425 430
 Met Asn Ala His Thr Gly Glu Leu Met Ala Val Lys Gln Val Glu Ile
 435 440 445
 Lys Asn Asn Asn Ile Gly Val Pro Thr Asp Asn Asn Lys Gln Ala Asn
 450 455 460
 Ser Asp Glu Asn Asn Glu Gln Glu Glu Gln Gln Glu Lys Ile Glu Asp
 465 470 475 480
 Val Gly Ala Val Ser His Pro Lys Thr Asn Gln Asn Ile His Arg Lys
 485 490 495
 Met Val Asp Ala Leu Gln His Glu Met Asn Leu Leu Lys Glu Leu His
 500 505 510
 His Glu Asn Ile Val Thr Tyr Tyr Gly Ala Ser Gln Glu Gly Gly Asn
 515 520 525
 Leu Asn Ile Phe Leu Glu Tyr Val Pro Gly Gly Ser Val Ser Ser Met
 530 535 540
 Leu Asn Asn Tyr Gly Pro Phe Glu Glu Ser Leu Ile Thr Asn Phe Thr
 545 550 555 560
 Arg Gln Ile Leu Ile Gly Val Ala Tyr Leu His Lys Lys Asn Ile Ile
 565 570 575
 His Arg Asp Ile Lys Gly Ala Asn Ile Leu Ile Asp Ile Lys Gly Cys
 580 585 590
 Val Lys Ile Thr Asp Phe Gly Ile Ser Lys Lys Leu Ser Pro Leu Asn
 595 600 605
 Lys Lys Gln Asn Lys Arg Ala Ser Leu Gln Gly Ser Val Phe Trp Met
 610 615 620
 Ser Pro Glu Val Val Lys Gln Thr Ala Thr Thr Ala Lys Ala Asp Ile
 625 630 635 640
 Trp Ser Thr Gly Cys Val Val Ile Gln Met Phe Thr Gly Lys His Pro
 645 650 655
 Phe Pro Asp Phe Ser Gln Met Gln Ala Ile Phe Lys Ile Gly Thr Asn
 660 665 670
 Thr Thr Pro Glu Ile Pro Ser Trp Ala Thr Ser Glu Gly Lys Asn Phe
 675 680 685
 Leu Arg Lys Ala Phe Glu Leu Asp Tyr Gln Tyr Arg Pro Ser Ala Leu
 690 695 700
 Glu Leu Leu Gln His Pro Trp Leu Asp Ala His Ile Ile

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705

710

715

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1478 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Pro Phe Leu Arg Lys Ile Ala Gly Thr Ala His Thr His Ser Arg
 1 5 10 15
 Ser Asp Ser Asn Ser Ser Val Lys Phe Gly His Gln Pro Thr Ser Ser
 20 25 30
 Val Ala Ser Thr Lys Ser Ser Ser Lys Ser Pro Arg Ala Thr Ser Arg
 35 40 45
 Lys Ser Ile Tyr Asp Asp Ile Arg Ser Gln Phe Pro Asn Leu Thr Pro
 50 55 60
 Asn Ser Thr Ser Ser Gln Phe Tyr Glu Ser Thr Pro Val Ile Glu Gln
 65 70 75 80
 Ser Phe Asn Trp Thr Thr Asp Asp His Ile Ser Ala Gly Thr Leu Glu
 85 90 95
 Asn Pro Thr Ser Glu Thr Asn Ser Ser Tyr Lys Asn Asp Asn Gly Pro
 100 105 110
 Ser Ser Leu Ser Asp Ser Arg Lys Ser Ser Gly Gly Asn Ser Val Asn
 115 120 125
 Ser Leu Ser Phe Asp Lys Leu Ile Leu Ser Trp Asp Pro Thr Asp Pro
 130 135 140
 Asp Glu Trp Thr Met His Arg Val Thr Ser Trp Phe Lys Phe His Asp
 145 150 155 160
 Phe Pro Glu Ser Trp Ile Leu Phe Phe Lys Lys His Gln Leu Phe Gly
 165 170 175
 His Arg Phe Ile Lys Leu Leu Ala Tyr Asp Asn Phe Ala Val Tyr Glu
 180 185 190
 Lys Tyr Leu Pro Gln Thr Lys Thr Ala Ser Tyr Thr Arg Phe Gln Gln
 195 200 205
 Leu Leu Lys Lys Thr Met Thr Lys Asn Val Thr Asn Ser His Ile Arg
 210 215 220
 Gln Lys Ser Ala Ser Lys Leu Lys Ser Ser Arg Ser Ser Ser Glu Ser
 225 230 235 240
 Ile Lys Ser Lys Leu Lys Asn Ser Lys Ser Gln Glu Asp Ile Ser Asn
 245 250 255
 Ser Arg Ser Thr Ser Glu Ser Ala Leu Ser Pro Thr Lys Ser Gly Pro
 260 265 270
 Ser Lys Thr Asp Glu Lys Asn Phe Leu His Ser Thr Ser Thr His Gln
 275 280 285

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Lys Thr Lys Ser Ala Ser Ser Leu Tyr Arg Arg Ser Phe Ile Ser Leu
 290 295 300
 Arg Gly Ser Ser Ser Ser Asn Ala Ser Ser Ala Lys Ser Pro Ser Asn
 305 310 315 320
 Ile Lys Leu Ser Ile Pro Ala Arg Pro His Ser Ile Ile Glu Ser Asn
 325 330 335
 Ser Thr Leu Thr Lys Ser Ala Ser Pro Pro Ala Ser Pro Ser Tyr Pro
 340 345 350
 Ser Ile Phe Arg Arg His His Lys Ser Ser Ser Ser Glu Ser Ser Leu
 355 360 365
 Ile Asn Ser Leu Phe Gly Ser Gly Ile Gly Glu Glu Ala Pro Thr Lys
 370 375 380
 Pro Asn Pro Gln Gly His Ser Leu Ser Ser Glu Asn Leu Ala Lys Gly
 385 390 395 400
 Lys Ser Lys His Tyr Glu Thr Asn Val Ser Ser Pro Leu Lys Gln Ser
 405 410 415
 Ser Leu Pro Thr Ser Asp Asp Lys Gly Asn Leu Trp Asn Lys Phe Lys
 420 425 430
 Arg Lys Ser Gln Ile Gly Val Pro Ser Pro Asn Thr Val Ala Tyr Val
 435 440 445
 Thr Ser Gln Glu Thr Pro Ser Leu Lys Ser Asn Ser Ser Thr Ala Thr
 450 455 460
 Leu Thr Val Gln Thr Ala Asp Val Asn Ile Pro Ser Pro Ser Ser Ser
 465 470 475 480
 Pro Pro Pro Ile Pro Lys Thr Ala Asn Arg Ser Leu Glu Val Ile Ser
 485 490 495
 Thr Glu Asp Thr Pro Lys Ile Ser Ser Thr Thr Ala Ser Phe Lys Glu
 500 505 510
 Thr Tyr Pro Asp Cys Ile Asn Pro Asp Lys Thr Val Pro Val Pro Val
 515 520 525
 Asn Asn Gln Lys Tyr Ser Val Lys Asn Phe Leu Leu Asp Gln Lys Phe
 530 535 540
 Tyr Pro Leu Lys Lys Thr Gly Leu Asn Asp Ser Glu Asn Lys Tyr Ile
 545 550 555 560
 Leu Val Thr Lys Asp Asn Val Ser Phe Val Pro Leu Asn Leu Lys Ser
 565 570 575
 Val Ala Lys Leu Ser Ser Phe Lys Glu Ser Ala Leu Thr Lys Leu Gly
 580 585 590
 Ile Asn His Lys Asn Val Thr Phe His Met Thr Asp Phe Asp Cys Asp
 595 600 605
 Ile Gly Ala Ala Ile Pro Asp Asp Thr Leu Glu Phe Leu Lys Lys Ser
 610 615 620
 Leu Phe Leu Asn Thr Ser Gly Lys Ile Tyr Ile Lys Asp Gln Met Lys
 625 630 635 640
 Leu Gln Gln Lys Pro Lys Pro Ala Pro Leu Thr Ser Glu Asn Asn Val

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645										650					655				
Pro	Leu	Lys	Ser	Val	Lys	Ser	Lys	Ser	Ser	Met	Arg	Ser	Gly	Thr	Ser				
			660						665					670					
Ser	Leu	Ile	Ala	Ser	Thr	Asp	Asp	Val	Ser	Ile	Val	Thr	Ser	Ser	Ser				
		675					680						685						
Asp	Ile	Thr	Ser	Phe	Asp	Glu	His	Ala	Ser	Gly	Ser	Gly	Arg	Arg	Tyr				
	690					695					700								
Pro	Gln	Thr	Pro	Ser	Tyr	Tyr	Tyr	Asp	Arg	Val	Ser	Asn	Thr	Asn	Pro				
705					710					715					720				
Thr	Glu	Glu	Leu	Asn	Tyr	Trp	Asn	Ile	Lys	Glu	Val	Leu	Ser	His	Glu				
				725					730					735					
Glu	Asn	Ala	Pro	Lys	Met	Val	Phe	Lys	Thr	Ser	Pro	Lys	Leu	Glu	Leu				
			740					745					750						
Asn	Ile	Pro	Asp	Lys	Gly	Ser	Lys	Leu	Asn	Ile	Pro	Thr	Pro	Ile	Thr				
		755					760					765							
Glu	Asn	Glu	Ser	Lys	Ser	Ser	Phe	Gln	Val	Leu	Arg	Lys	Asp	Glu	Gly				
	770					775					780								
Thr	Glu	Ile	Asp	Phe	Asn	His	Arg	Arg	Glu	Ser	Pro	Tyr	Thr	Lys	Pro				
735					790					795					800				
Glu	Leu	Ala	Pro	Lys	Arg	Glu	Ala	Pro	Lys	Pro	Pro	Ala	Asn	Thr	Ser				
			805						810					815					
Pro	Gln	Arg	Thr	Leu	Ser	Thr	Ser	Lys	Gln	Asn	Lys	Pro	Ile	Arg	Leu				
			820					825					830						
Val	Arg	Ala	Ser	Thr	Lys	Ile	Ser	Arg	Ser	Lys	Arg	Ser	Lys	Pro	Leu				
		835					840					845							
Pro	Pro	Gln	Leu	Leu	Ser	Ser	Pro	Ile	Glu	Ala	Ser	Ser	Ser	Ser	Pro				
	850					855					860								
Asp	Ser	Leu	Thr	Ser	Ser	Tyr	Thr	Pro	Ala	Ser	Thr	His	Val	Leu	Ile				
865					870					875					880				
Pro	Gln	Pro	Tyr	Lys	Gly	Ala	Asn	Asp	Val	Met	Arg	Arg	Leu	Lys	Thr				
				885					890					895					
Asp	Gln	Asp	Ser	Thr	Ser	Thr	Ser	Pro	Ser	Leu	Lys	Met	Lys	Gln	Lys				
			900					905					910						
Val	Asn	Arg	Ser	Asn	Ser	Thr	Val	Ser	Thr	Ser	Asn	Ser	Ile	Phe	Tyr				
		915					920					925							
Ser	Pro	Ser	Pro	Leu	Leu	Lys	Arg	Gly	Asn	Ser	Lys	Arg	Val	Val	Ser				
	930					935					940								
Ser	Thr	Ser	Ala	Ala	Asp	Ile	Phe	Glu	Glu	Asn	Asp	Ile	Thr	Phe	Ala				
945					950					955					960				
Asp	Ala	Pro	Pro	Met	Phe	Asp	Ser	Asp	Asp	Ser	Asp	Asp	Asp	Ser	Ser				
				965					970					975					
Ser	Ser	Asp	Asp	Ile	Ile	Trp	Ser	Lys	Lys	Lys	Thr	Ala	Pro	Glu	Thr				
				980				985					990						
Asn	Asn	Glu	Asn	Lys	Lys	Asp	Glu	Lys	Ser	Asp	Asn	Ser	Ser	Thr	His				
		995					1000					1005							

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cont

Ser Asp Glu Ile Phe Tyr Asp Ser Gln Thr Gln Asp Lys Met Glu Arg
 1010 1015 1020
 Lys Met Thr Phe Arg Pro Ser Pro Glu Val Val Tyr Gln Asn Leu Glu
 1025 1030 1035 1040
 Lys Phe Phe Pro Arg Ala Asn Leu Asp Lys Pro Ile Thr Glu Gly Ile
 1045 1050 1055
 Ala Ser Pro Thr Ser Pro Lys Ser Leu Asp Ser Leu Leu Ser Pro Lys
 1060 1065 1070
 Asn Val Ala Ser Ser Arg Thr Glu Pro Ser Thr Pro Ser Arg Pro Val
 1075 1080 1085
 Pro Pro Asp Ser Ser Tyr Glu Phe Ile Gln Asp Gly Leu Asn Gly Lys
 1090 1095 1100
 Asn Lys Pro Leu Asn Gln Ala Lys Thr Pro Lys Arg Thr Lys Thr Ile
 1105 1110 1115 1120
 Arg Thr Ile Ala His Glu Ala Ser Leu Ala Arg Lys Asn Ser Val Lys
 1125 1130 1135
 Leu Lys Arg Gln Asn Thr Lys Met Trp Gly Thr Arg Met Val Glu Val
 1140 1145 1150
 Thr Glu Asn His Met Val Ser Ile Asn Lys Ala Lys Asn Ser Lys Gly
 1155 1160 1165
 Glu Tyr Lys Glu Phe Ala Trp Met Lys Gly Glu Met Ile Gly Lys Gly
 1170 1175 1180
 Ser Phe Gly Ala Val Tyr Leu Cys Leu Asn Val Thr Thr Gly Glu Met
 1185 1190 1195 1200
 Met Ala Val Lys Gln Val Glu Val Pro Lys Tyr Ser Ser Gln Asn Glu
 1205 1210 1215
 Ala Ile Leu Ser Thr Val Glu Ala Leu Arg Ser Glu Val Ser Thr Leu
 1220 1225 1230
 Lys Asp Leu Asp His Leu Asn Ile Val Gln Tyr Leu Gly Phe Glu Asn
 1235 1240 1245
 Lys Asn Asn Ile Tyr Ser Leu Phe Leu Glu Tyr Val Ala Gly Gly Ser
 1250 1255 1260
 Val Gly Ser Leu Ile Arg Met Tyr Gly Arg Phe Asp Glu Pro Leu Ile
 1265 1270 1275 1280
 Lys His Leu Thr Thr Gln Val Leu Lys Gly Leu Ala Tyr Leu His Ser
 1285 1290 1295
 Lys Gly Ile Leu His Arg Asp Met Lys Ala Asp Asn Leu Leu Leu Asp
 1300 1305 1310
 Gln Asp Gly Ile Cys Lys Ile Ser Asp Phe Gly Ile Ser Arg Lys Ser
 1315 1320 1325
 Lys Asp Ile Tyr Ser Asn Ser Asp Met Thr Met Arg Gly Thr Val Phe
 1330 1335 1340
 Trp Met Ala Pro Glu Met Val Asp Thr Lys Gln Gly Tyr Ser Ala Lys
 1345 1350 1355 1360
 Val Asp Ile Trp Ser Leu Gly Cys Ile Val Leu Glu Met Phe Ala Gly

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1365							1370					1375				
Lys	Arg	Pro	Trp	Ser	Asn	Leu	Glu	Val	Val	Ala	Ala	Met	Phe	Lys	Ile	
1380							1385					1390				
Gly	Lys	Ser	Lys	Ser	Ala	Pro	Pro	Ile	Pro	Glu	Asp	Thr	Leu	Pro	Leu	
1395							1400					1405				
Ile	Ser	Gln	Ile	Gly	Arg	Asn	Phe	Leu	Asp	Ala	Cys	Phe	Glu	Ile	Asn	
1410							1415					1420				
Pro	Glu	Lys	Arg	Pro	Thr	Ala	Asn	Glu	Leu	Leu	Ser	His	Pro	Phe	Ser	
1425							1430					1435				
Glu	Val	Asn	Glu	Thr	Phe	Asn	Phe	Lys	Ser	Thr	Arg	Leu	Ala	Lys	Phe	
1445							1450					1455				
Ile	Lys	Ser	Asn	Asp	Lys	Leu	Asn	Ser	Ser	Lys	Leu	Arg	Ile	Thr	Ser	
1460							1465					1470				
Gln	Glu	Asn	Lys	Thr	Glu											
1475																

(2) INFORMATION FOR SEQ ID NO 19:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 687 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID/NO:19:

Met 1	Val	Gly	Lys	Leu 5	Ser	Arg	Arg	Ile	Tyr 10	Leu	Ser	Ser	Ala	Arg 15	Met
Val	Thr	Ala	Val 20	Pro	Ala	Val	Phe	Ser 25	Lys	Leu	Val	Thr	Met 30	Leu	Asn
Ala	Ser	Gly 35	Ser	Thr	His	Phe	Thr 40	Arg	Met	Arg	Arg	Arg	Leu	Met	Ala
Ile	Ala	Asp 50	Glu	Val	Glu	Ile 55	Ala	Glu	Val	Ile	Gln	Leu	Gly	Val	Glu
Asp 65	Thr	Val	Asp	Gly	His 70	Gln	Asp	Ser	Leu	Gln 75	Ala	Val	Ala	Pro	Thr 80
Ser	Cys	Leu	Glu	Asn 85	Ser	Ser	Leu	Glu	His 90	Thr	Val	His	Arg	Glu 95	Lys
Thr	Gly	Lys	Gly 100	Leu	Ser	Ala	Thr	Arg 105	Leu	Ser	Ala	Ser	Ser	Glu	Asp
Ile	Ser	Asp 115	Arg	Leu	Ala	Gly	Val 120	Ser	Val	Gly	Leu	Pro 125	Ser	Ser	Thr
Thr	Thr 130	Glu	Gln	Pro	Lys	Pro 135	Ala	Val	Gln	Thr	Lys 140	Gly	Arg	Pro	His
Ser 145	Gln	Cys	Leu	Asn 150	Ser	Ser	Pro	Leu	Ser	His 155	Ala	Gln	Leu	Met	Phe 160
Pro	Ala	Pro	Ser	Ala 165	Pro	Cys	Ser	Ser	Ala 170	Pro	Ser	Val	Pro	Asp 175	Ile

Sub
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Ser Lys His Arg Pro Gln Ala Phe Val Pro Cys Lys Ile Pro Ser Ala
 180 185 190
 Ser Pro Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe Gln Arg Asn Cys
 195 200 205
 Ser Glu His Arg Asp Ser Asp Gln Leu Ser Pro Val Phe Thr Gln Ser
 210 215 220
 Arg Pro Pro Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg Pro
 225 230 235 240
 Val Pro Gly Ser Thr Ser Lys Leu Gly Asp Ala Thr Lys Ser Ser Met
 245 250 255
 Thr Leu Asp Leu Gly Ser Ala Ser Arg Cys Asp Asp Ser Phe Gly Gly
 260 265 270
 Gly Gly Asn Ser Gly Asn Ala Val Ile Pro Ser Asp Glu Thr Val Phe
 275 280 285
 Thr Pro Val Glu Asp Lys Cys Arg Leu Asp Val Asn Thr Glu Leu Asn
 290 295 300
 Ser Ser Ile Glu Asp Leu Leu Glu Ala Ser Met Pro Ser Ser Asp Thr
 305 310 315 320
 Thr Val Thr Phe Lys Ser Glu Val Ala Val Leu Ser Pro Glu Lys Ala
 325 330 335
 Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys Cys
 340 345 350
 Lys Glu Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile Ala Met
 355 360 365
 Ala Met Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu Gln
 370 375 380
 Val Glu Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro Glu
 385 390 395 400
 Thr Leu Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp Ala
 405 410 415
 Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser Cys
 420 425 430
 Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys Gln
 435 440 445
 Val Thr Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val Val Glu
 450 455 460
 Ala Leu Arg Glu Glu Ile Arg Met Met Gly His Leu Asn His Pro Asn
 465 470 475 480
 Ile Ile Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu
 485 490 495
 Phe Ile Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser Lys
 500 505 510
 Tyr Gly Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln Leu
 515 520 525
 Leu Arg Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp

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530	535	540
Val Lys Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg		
545	550	555
Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly		
	565	570
Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met Ala		
	580	585
Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp		
	595	600
Ser Val Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro Trp		
	610	615
Asn Ala Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys Ile Ala		
	625	630
Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly Leu		
	645	650
Arg Asp Val Ala Val Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro		
	660	665
Pro Ser Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp		
	675	680

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1314 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Met Met Asp Ile Leu Asn Thr Gln Gln Gln Lys Ala Ala Glu Gly		
1	5	10
Gly Arg Val Leu Ala Pro His Thr Ile Ser Ser Lys Leu Val Lys Arg		
	20	25
Leu Ser Ser His Ser Ser His Lys Leu Ser Arg Ser Asp Leu Lys Ala		
	35	40
Leu Gly Gly Ser Glu Thr Ile Ser Asp Gly Pro Ser Gln Leu Thr Phe		
	50	55
Lys Asp Arg Tyr Val Phe Asn Glu Ser Leu Tyr Leu Lys Lys Leu Lys		
	65	70
Lys Thr Ala Leu Asp Asp Tyr Tyr Thr Arg Gly Ile Lys Leu Thr Asn		
	85	90
Arg Tyr Glu Glu Asp Asp Gly Asp Asp Glu Ile Ile Arg Leu Ser Asn		
	100	105
Gly Asp Arg Ile Asp Glu Asp Leu His Ser Gly Val Lys Phe Phe Ser		
	115	120
Thr Thr Pro Tyr Cys Arg Lys Met Arg Ser Asp Ser Asp Glu Leu Ala		
	130	135

Sub
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cont.

Trp Asn Glu Ile Ala Thr Glu Arg Phe Lys Trp Gln Ser Met Leu Ala
 145 150 155 160
 Arg Val Leu Lys Gly Asp Ile Val Lys Gly Glu Lys Thr Arg Ile Ala
 165 170 175
 Asn Gln Val Lys Lys Pro Gly Leu Asn Lys Glu Leu Ser Asp Glu Ile
 180 185 190
 Trp Leu Glu Leu Lys Ala Trp Leu Asn Gly Arg Thr Met Gln Glu Met
 195 200 205
 Glu Gln Ser Leu Thr Tyr Leu Arg Asp Ser Ser Asp Ser Val Phe Glu
 210 215 220
 Glu Ile Met Lys Phe Gln Ile Pro Gln Gly Lys Ile Leu Ser Leu Asp
 225 230 235 240
 Ala Leu Glu Ala Ile Leu Gln Asp Leu Met Asn Arg Tyr His Ser Val
 245 250 255
 Val Ser Tyr Trp Pro Asn Leu Lys Lys Met Tyr Lys Asp Lys Pro Ile
 260 265 270
 Thr Asn Thr Ala Glu Phe Thr Ala Arg Ile Asp Val Met Asn Ser Trp
 275 280 285
 Leu Asn Phe Lys Thr Asn Leu Thr Leu Arg Arg Gln Glu Leu Asp Asp
 290 295 300
 Trp Ile Asn Arg Phe Ser Pro Ile Ser Ser Ser Asp Asn Cys Gln Glu
 305 310 315 320
 Asp Phe Asp Gly Val Pro Gln Trp Asn Cys Lys Met Lys Ile Leu Ala
 325 330 335
 Glu Gln Leu Met Lys Glu Lys Asn Ile Glu Ser Ile Phe Gln Lys Lys
 340 345 350
 Ile Phe Tyr Pro Leu Ser Pro Trp Met Phe Lys Leu Lys Leu His Phe
 355 360 365
 Ile Val Tyr Arg Glu Thr Leu Thr Lys Met Asn Ile Lys Tyr Pro Tyr
 370 375 380
 Glu Arg Leu Arg Ser Leu Leu Ala Phe Pro Val Tyr Leu Ile Lys Glu
 385 390 395 400
 Val Ile Leu Thr Arg Leu Ser Tyr Ala Arg Lys Leu Lys Asn Pro Thr
 405 410 415
 Met Met Met Ile Asp Gln Met Ile Asp Asp Phe Asn Ala Phe Ile Arg
 420 425 430
 Leu Ser Val Gln Leu Lys Tyr Thr Leu Thr Lys Tyr Cys Ser Asn Leu
 435 440 445
 Pro Phe Asp Val Asp Phe Asp Pro Thr Phe Glu Asn Thr Val Ile Glu
 450 455 460
 Ala Ile Arg Tyr Leu Phe Phe Leu Leu Asn Leu Lys Leu Ile Asp Ser
 465 470 475 480
 Ser Lys Gln Asn Phe Lys Ala Pro Asp Leu Leu Leu Lys Tyr Trp Asp
 485 490 495
 His Leu Lys Asn Thr Gly His Tyr Ile Asn Gly Ala Glu Thr Val Ile

Sub
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500										505					510				
Pro	Asn	Glu	Phe	Leu	Lys	Leu	Thr	Leu	Arg	Leu	Val	His	Lys	Leu	Gln				
	515						520					525							
Phe	Tyr	Leu	Leu	Lys	Gln	Gln	Asn	Phe	Pro	Pro	Thr	Phe	Ala	Asn	Ala				
	530					535					540								
Ser	Glu	Ala	Glu	Lys	Trp	Leu	Ser	Ser	Ile	Phe	Glu	Asn	Leu	Gly	Ala				
545					550					555					560				
Met	Lys	Arg	Lys	Leu	Asn	Arg	Phe	Ser	Asn	Ile	Leu	Val	Lys	Ala	Phe				
				565					570					575					
Gln	Asn	Ser	Ala	Val	Tyr	Gln	Ile	Asn	His	Asn	Ala	Gln	Leu	Val	Lys				
			580					585					590						
Lys	Leu	Lys	Asp	Ala	His	Tyr	Phe	Leu	Val	Tyr	Ser	Gly	Asn	Thr	Phe				
		595					600					605							
Glu	Ser	Ser	Gly	Val	Tyr	Met	Phe	Ala	Ala	Pro	Glu	Leu	Leu	Gly	Cys				
	610					615					620								
Asp	Asn	Asp	Thr	Ile	Leu	Arg	Ile	Leu	Arg	Asn	Lys	Ser	Ile	Gly	Cys				
625					630					635					640				
Asp	Leu	Val	Pro	Lys	Leu	Asp	Ile	Gly	Asn	Asn	Leu	Asn	Val	Tyr	Asp				
				645					650					655					
Ile	Thr	Thr	Lys	Glu	Thr	Asp	Leu	Asn	Ile	Leu	Val	Ser	Lys	Gly	Glu				
			660					665					670						
Asp	Ser	Lys	Gly	Ile	Pro	Tyr	Tyr	Arg	Val	Val	Ala	Asn	Ser	Ser	Ser				
		675					680					685							
Asp	Leu	Asp	Arg	His	Ala	His	Gln	Ser	Lys	Lys	Lys	Asn	Phe	Ser	Thr				
	690					695						700							
Asp	Pro	Phe	Asp	Gln	His	Leu	Asp	Glu	Lys	Asn	Asn	Glu	Val	Phe	Glu				
705					710					715					720				
Leu	Glu	Val	Ala	Leu	Ser	Ser	Leu	Gly	Ala	Leu	Val	Val	Leu	Tyr	Pro				
				725					730					735					
Gly	Glu	Pro	Val	Val	Trp	Asp	Gly	Pro	Val	Tyr	Lys	Leu	Pro	Gly	Asn				
			740					745					750						
Asn	Leu	Phe	Ala	Ser	Asn	Glu	Met	Asp	Leu	Gly	Lys	Ile	Gly	Asn	Pro				
		755					760					765							
Asn	Thr	Leu	Ile	Leu	Leu	Asn	Gln	Gly	Ser	Asn	Tyr	Ala	Leu	Thr	Tyr				
		770				775					780								
Gln	Ile	Asp	Lys	Phe	Asn	Gln	Thr	Val	Gly	Asp	Ser	Val	Ser	Phe	Ile				
785					790					795					800				
Glu	Lys	Arg	Cys	Ser	Leu	Asn	Ser	Ile	Glu	Ser	Ser	Leu	Gln	Lys	Ile				
				805					810					815					
Asn	Lys	Ala	Tyr	Tyr	Lys	Leu	Thr	Tyr	Thr	Val	Leu	Asn	Asn	Tyr	Lys				
			820					825					830						
Gly	Ile	Leu	Gly	Ser	Phe	Met	Lys	Gln	Cys	Pro	Gly	Asn	Glu	Leu	Leu				
		835					840					845							
Asn	Ser	Ile	Phe	Met	Phe	Gly	Arg	Asp	Phe	Gly	Arg	Ser	Phe	Leu	Lys				
	850					855					860								

*Sub
D1
anti-*

Tyr Asn Ala Phe Ser Ser Lys Arg Lys Tyr Val Ile Ile Phe Leu Met
 865 870 875 880
 Val Lys Leu Gly Met Asn Trp Leu Lys Phe Leu Val Glu Glu Cys Asp
 885 890 895
 Pro Thr Asp Gln Arg Thr Phe Arg Trp Cys Val Leu Ala Met Asp Phe
 900 905 910
 Ala Met Gln Met Thr Ser Gly Tyr Asn Ile Leu Ala Leu Asn Val Lys
 915 920 925
 Gln Phe Gln Glu Leu Lys Glu Arg Val Ser Val Cys Met Ser Leu Leu
 930 935 940
 Ile Ser His Phe Asp Val Met Gly Ala Arg Ala Thr Glu Ala Glu Asn
 945 950 955 960
 Gly Met Gln Gln Ala Arg Leu Asn Ile Asp Thr Glu Glu Asn Ile Asp
 965 970 975
 Glu Glu Ala Thr Leu Glu Ile Asn Ser Arg Leu Arg Leu Glu Ala Ile
 980 985 990
 Lys Thr Leu Glu Lys Thr Met Lys Arg Asn Pro Arg Gln Met Gly Lys
 995 1000 1005
 Val Leu Asp Ala Thr Asp Gln Gly Asn Lys Tyr Leu Leu Ser Leu Ala
 1010 1015 1020
 Ser Ser Leu Ser Asn Val Ser Met Arg Trp Gln Lys Arg Ser Phe Ile
 1025 1030 1035 1040
 Gly Gly Gly Thr Phe Gly Gln Val Tyr Ser Ala Ile Asn Leu Glu Asn
 1045 1050 1055
 Gly Glu Ile Leu Ala Val Lys Glu Ile Lys Ile His Asp Thr Thr Thr
 1060 1065 1070
 Met Lys Lys Ile Phe Pro Leu Ile Lys Glu Glu Met Thr Val Leu Glu
 1075 1080 1085
 Met Leu Asn His Pro Asn Ile Val Gln Tyr Tyr Gly Val Glu Val His
 1090 1095 1100
 Arg Asp Lys Val Asn Ile Phe Met Glu Tyr Cys Glu Gly Gly Ser Leu
 1105 1110 1115 1120
 Ala Ser Leu Leu Asp His Gly Arg Ile Glu Asp Glu Met Val Thr Gln
 1125 1130 1135
 Val Tyr Thr Phe Glu Leu Leu Glu Gly Leu Ala Tyr Leu His Gln Ser
 1140 1145 1150
 Gly Val Val His Arg Asp Ile Lys Pro Glu Asn Ile Leu Leu Asp Phe
 1155 1160 1165
 Asn Gly Ile Ile Lys Tyr Val Asp Phe Gly Thr Ala Arg Thr Val Val
 1170 1175 1180
 Gly Ser Arg Thr Arg Thr Val Arg Asn Ala Ala Val Gln Asp Phe Gly
 1185 1190 1195 1200
 Val Glu Thr Lys Ser Leu Asn Glu Met Met Gly Thr Pro Met Tyr Met
 1205 1210 1215
 Ala Pro Glu Thr Ile Ser Gly Ser Ala Val Lys Gly Lys Leu Gly Ala

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1220

1225

1230

Asp Asp Val Trp Ala Leu Gly Cys Val Val Leu Glu Met Ala Thr Gly
1235 1240 1245

Arg Arg Pro Trp Ser Asn Leu Asp Asn Glu Trp Ala Ile Met Tyr His
1250 1255 1260

Val Ala Ala Gly Arg Ile Pro Gln Leu Pro Asn Arg Asp Glu Met Thr
1265 1270 1275 1280

Ala Ala Gly Arg Ala Leu Leu Gly Lys Val Phe Gly Ser Arg Pro His
1285 1290 1295

Tyr Glu Gly Tyr Cys Cys Gly Thr Thr Asp Arg Pro Leu Asp Asp Thr
1300 1305 1310

Asn Pro

Sub
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C2 cont
concluded